TEG1

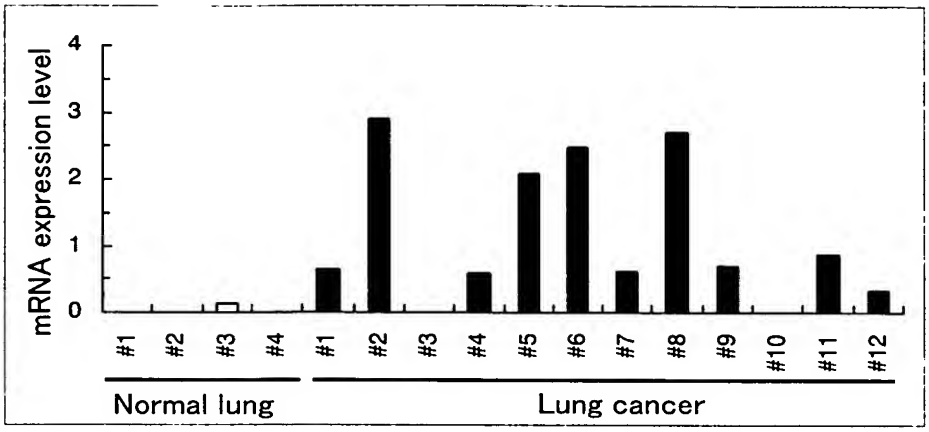

FIG. 1

TEG2(Large bowel cancer)

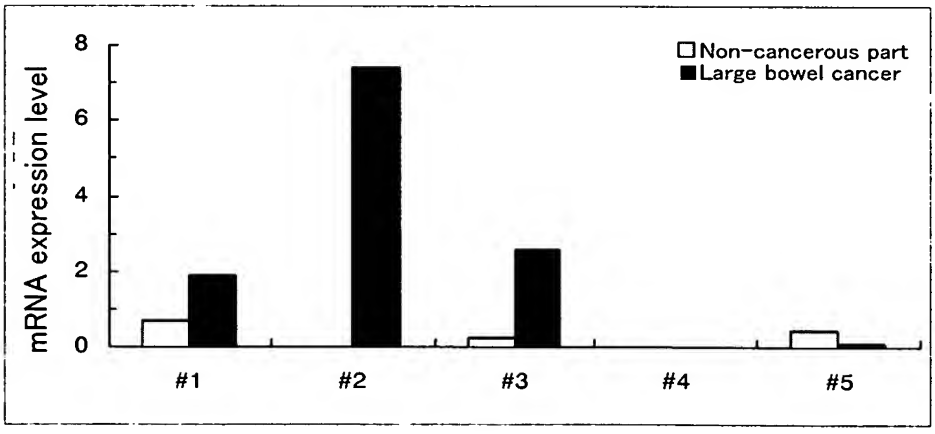

FIG. 2

TEG2 (Stomach cancer)

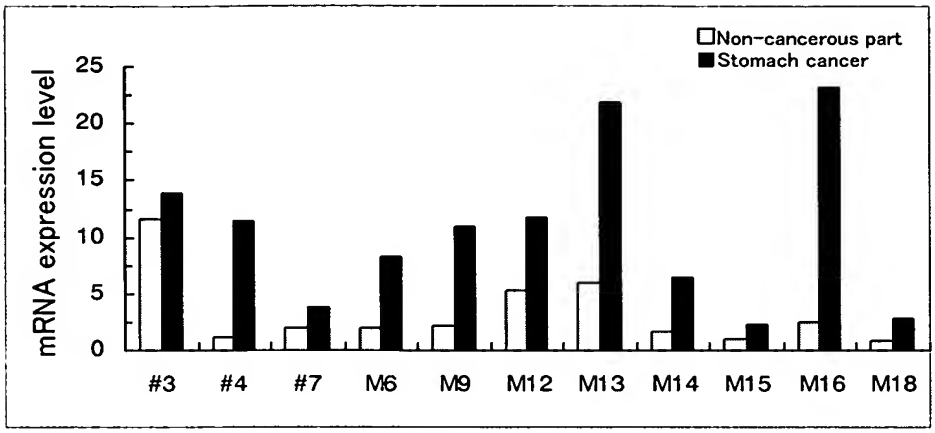

FIG. 3

TEG3

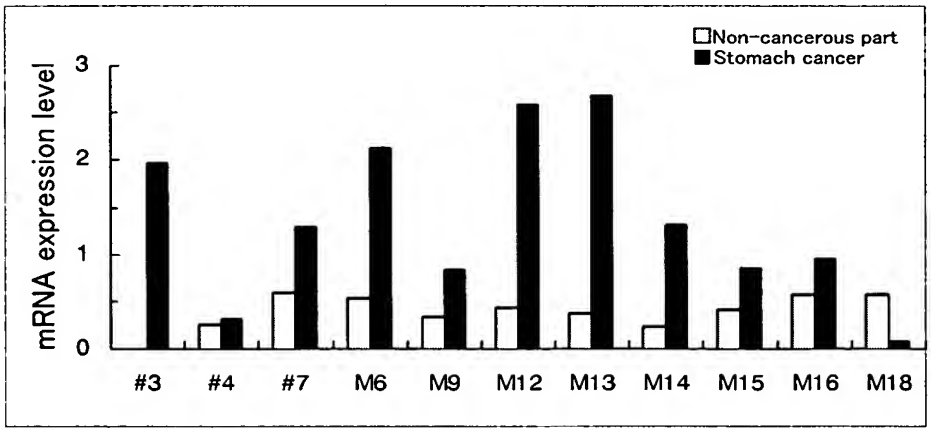

FIG. 4

TEG4

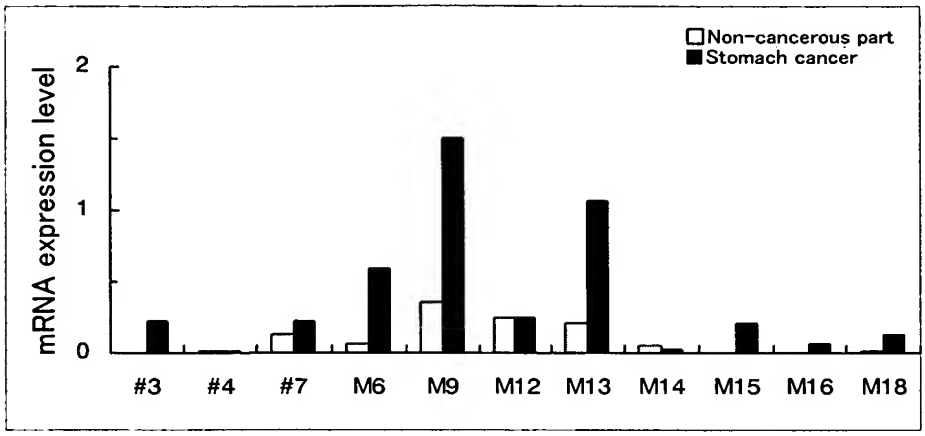

FIG. 5

TEG5

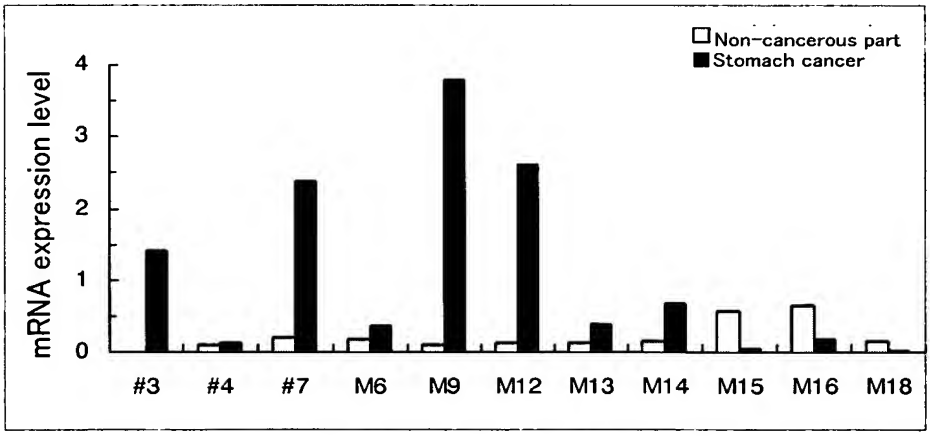

FIG. 6

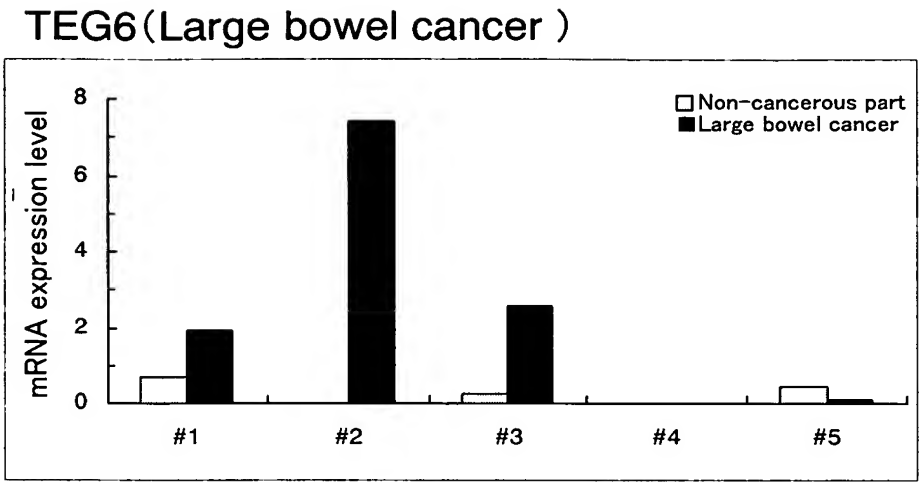
TEG6(Large bowel cancer)
mRNA expression level
8
6
4
2
0
Non-cancerous part
Large bowel cancer
#1
#2
#3
#4
#5

FIG. 7

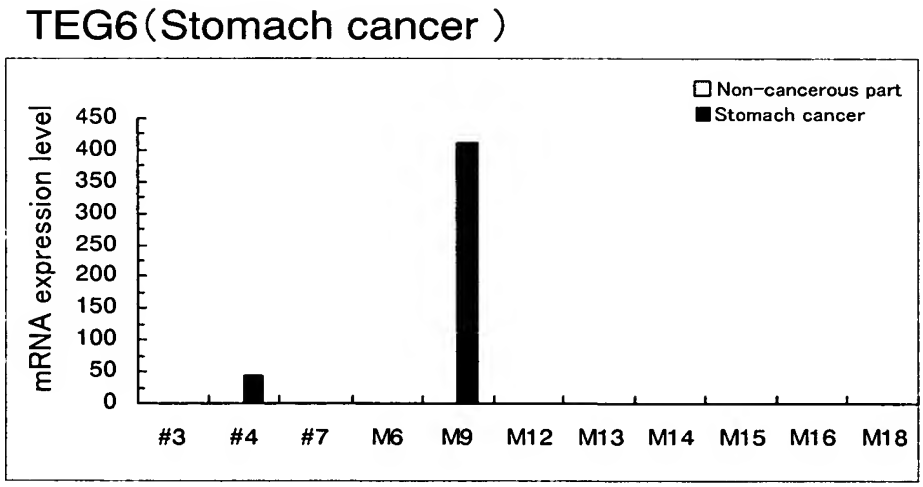
TEG6(Stomach cancer)
mRNA expression level
450
400
350
300
250
200
150
100
50
0
Non-cancerous part
Stomach cancer
#3
#4
#7
M6
M9
M12
M13
M14
M15
M16
M18

FIG. 8

TEG7

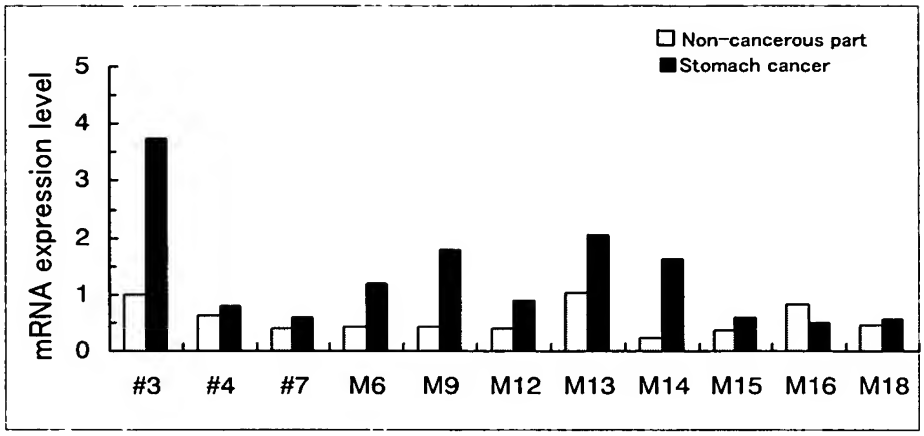

FIG. 9

TEG8

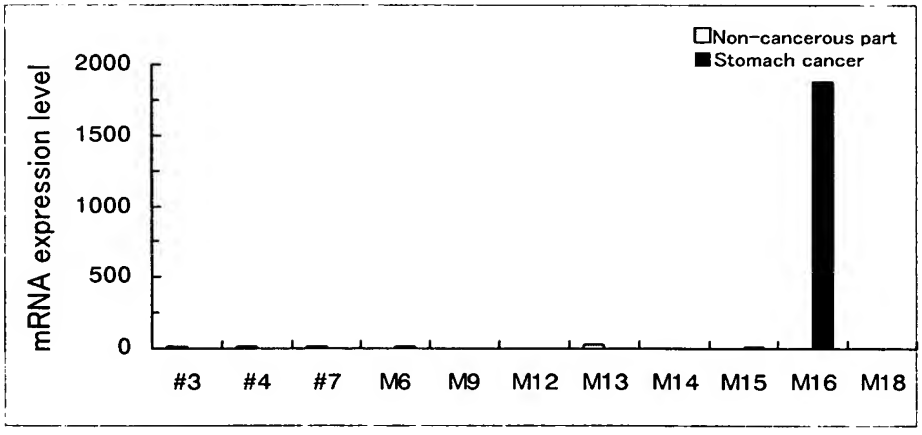

FIG. 10

TEG9

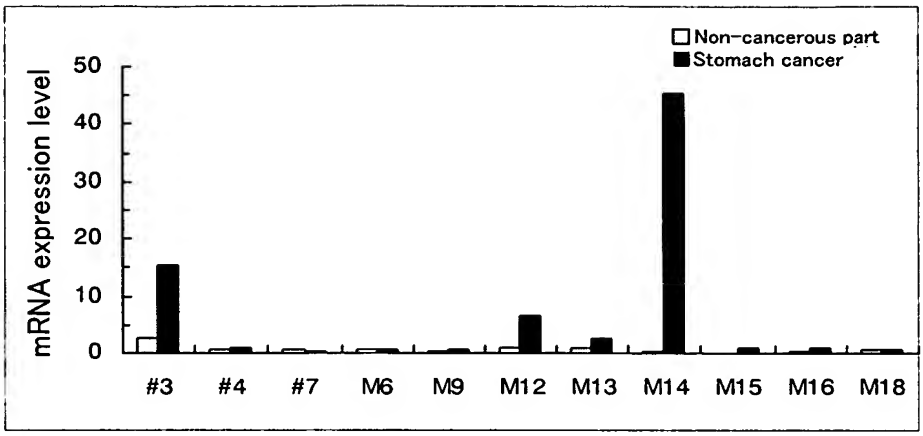

FIG. 11

TEG10

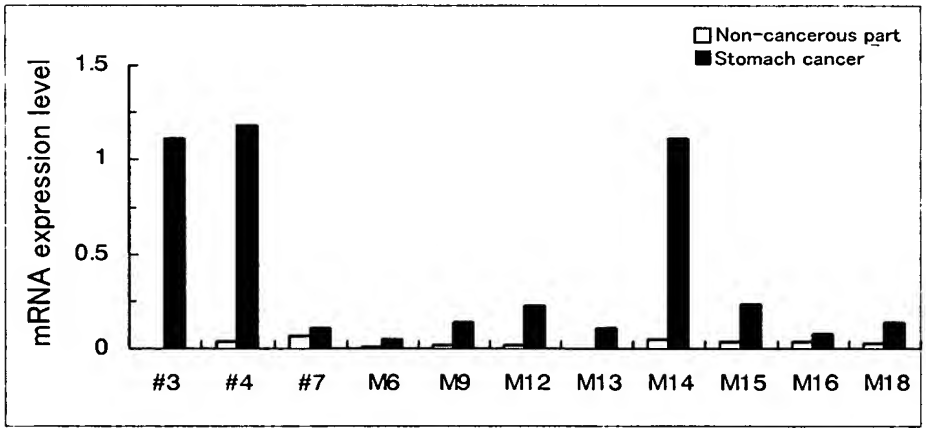

FIG.12

TEG11

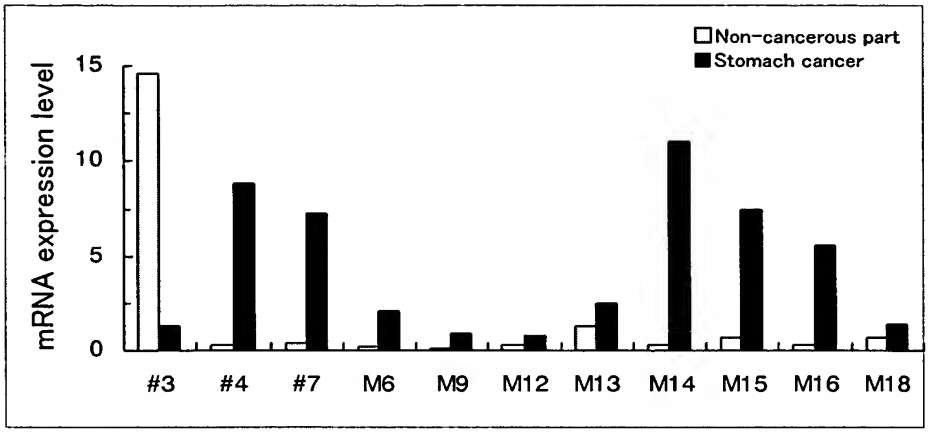

FIG. 13

TEG12

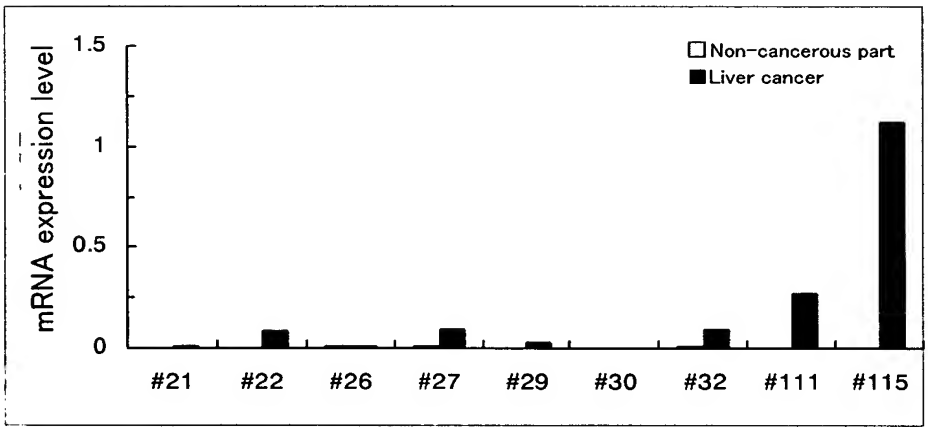

FIG. 14

TEG13

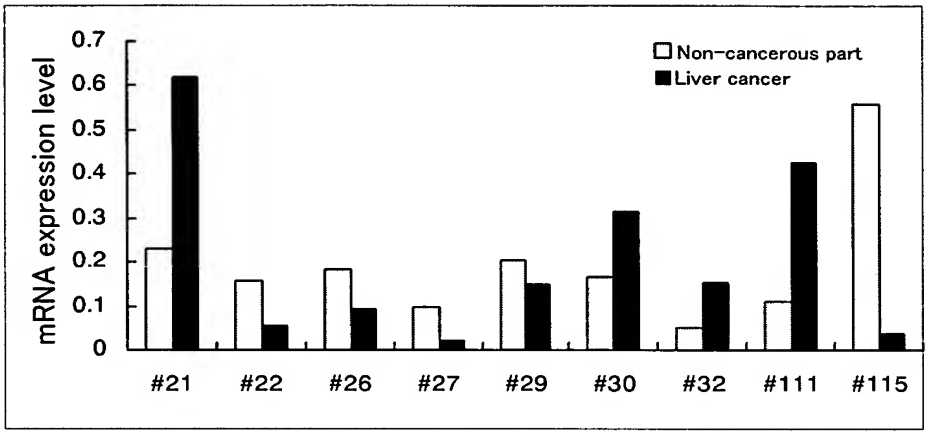

FIG. 15

TEG14

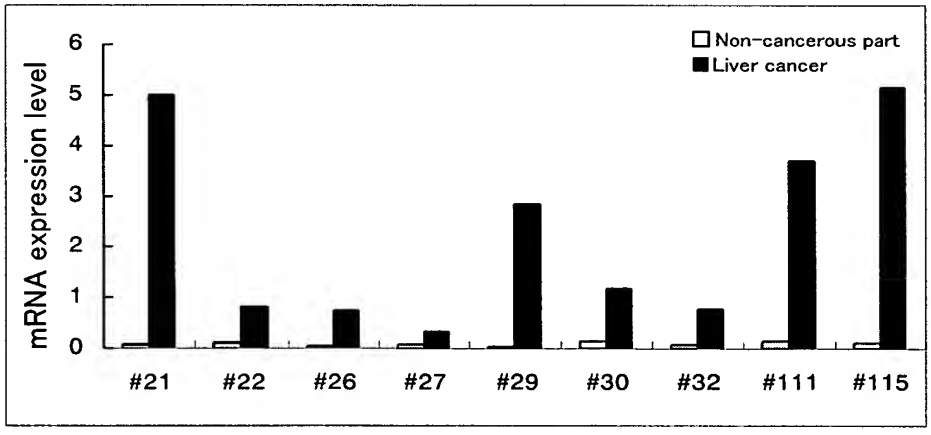

FIG. 16

TEG15

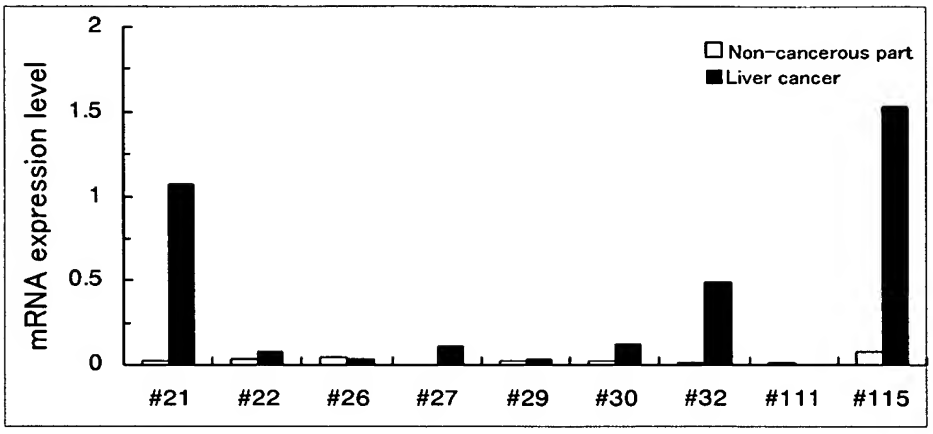

FIG. 17

TEG16

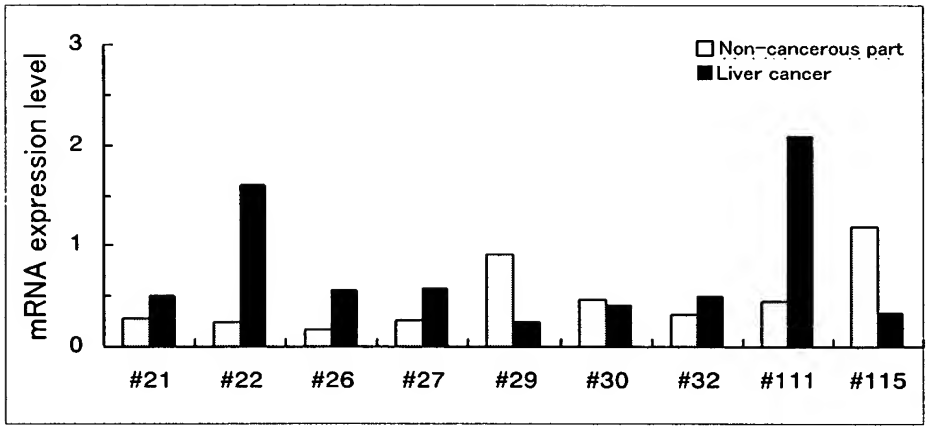

FIG. 18

TEG17

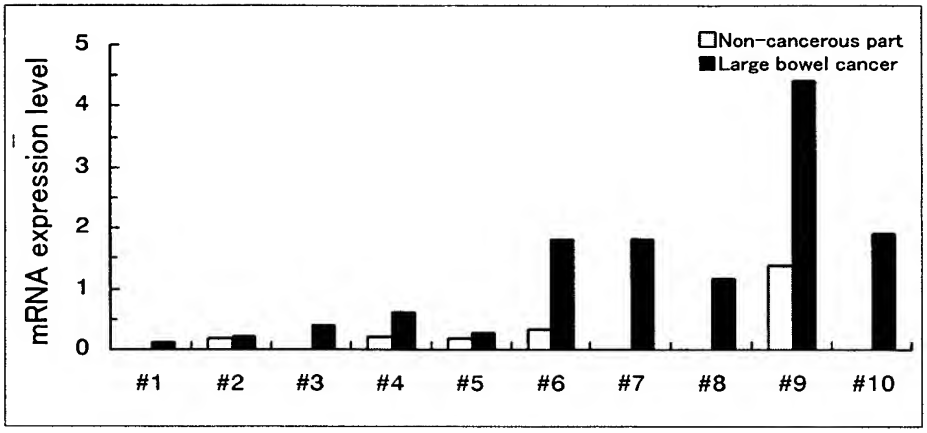

FIG. 19

TEG18

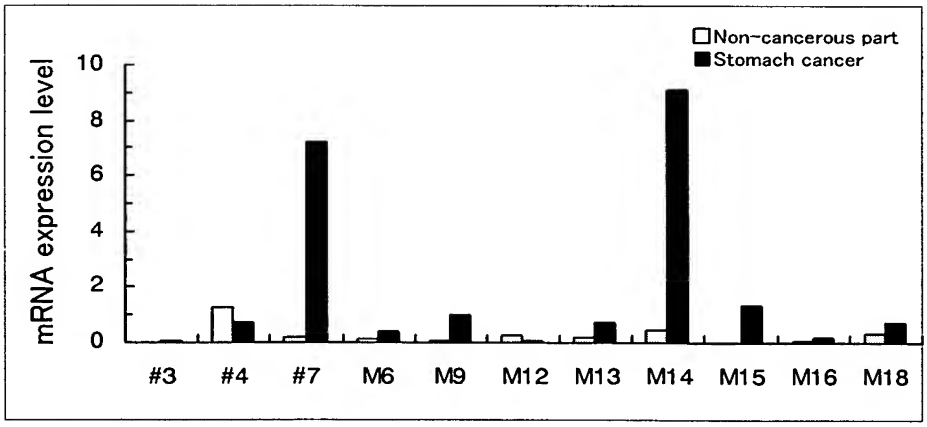

FIG. 20

TEG19

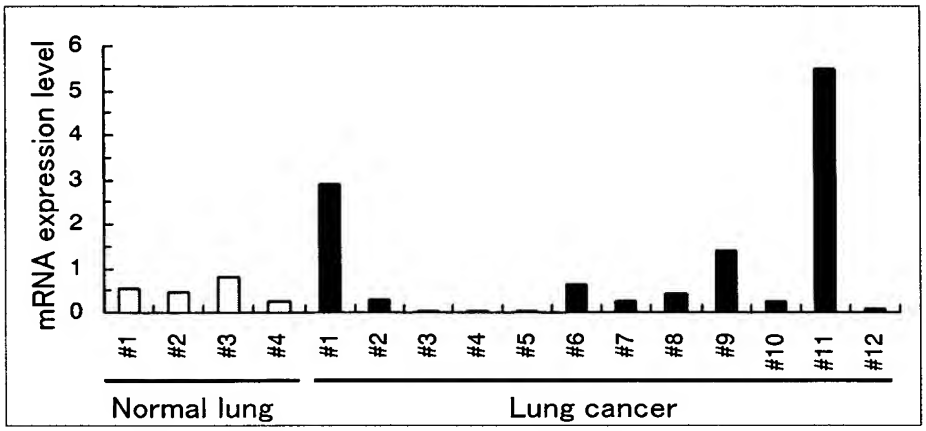

FIG. 21

TEG20

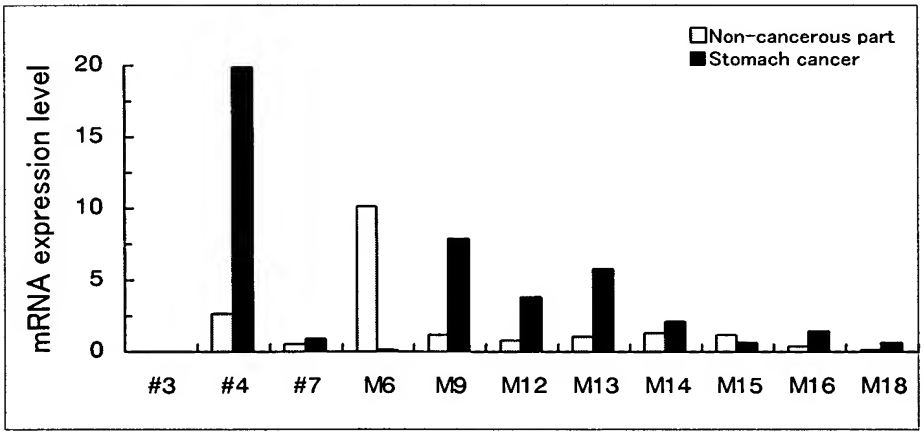

FIG. 22

TEG21

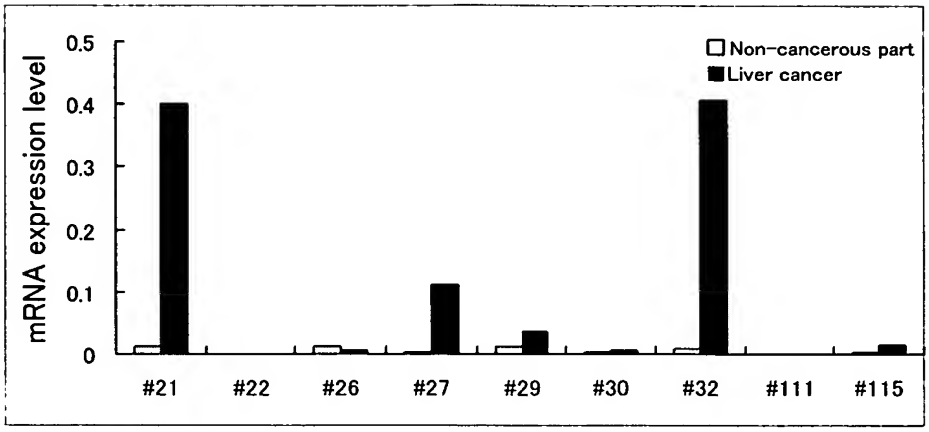

FIG. 23

TEG22

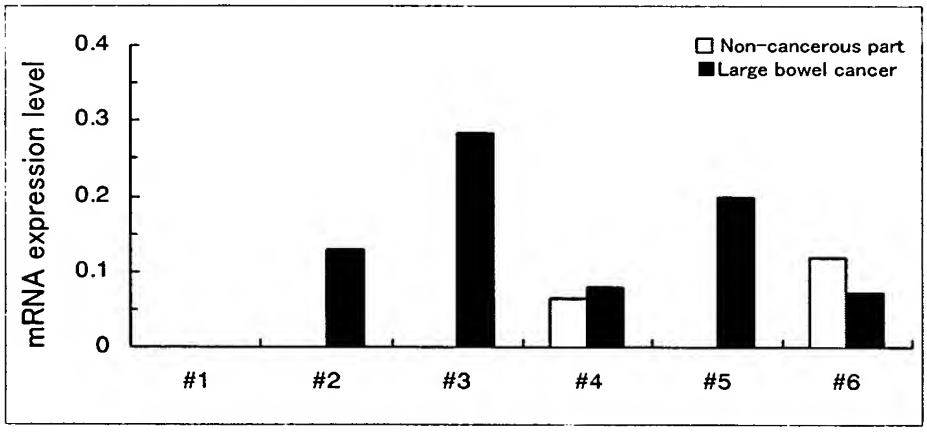

FIG. 24

TEG23

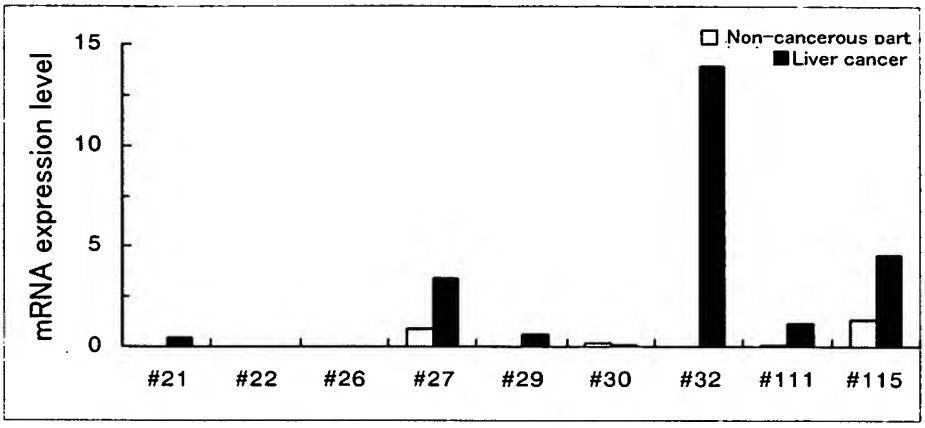

FIG. 25

TEG24

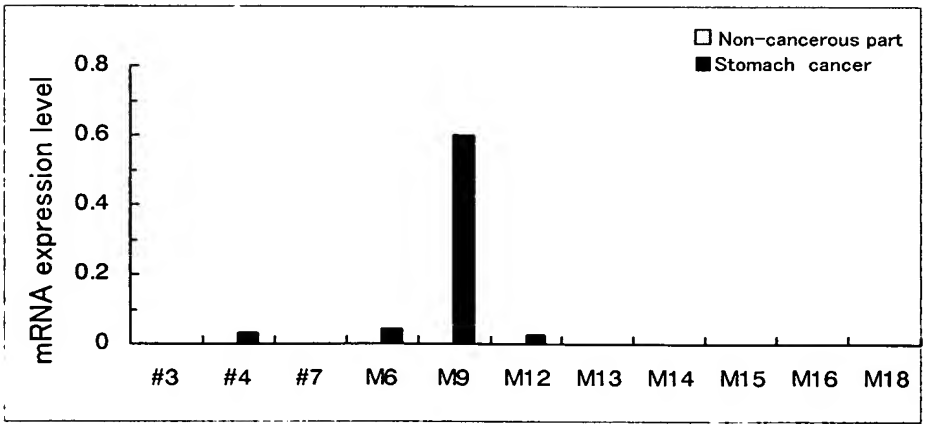

FIG. 26

TEG25

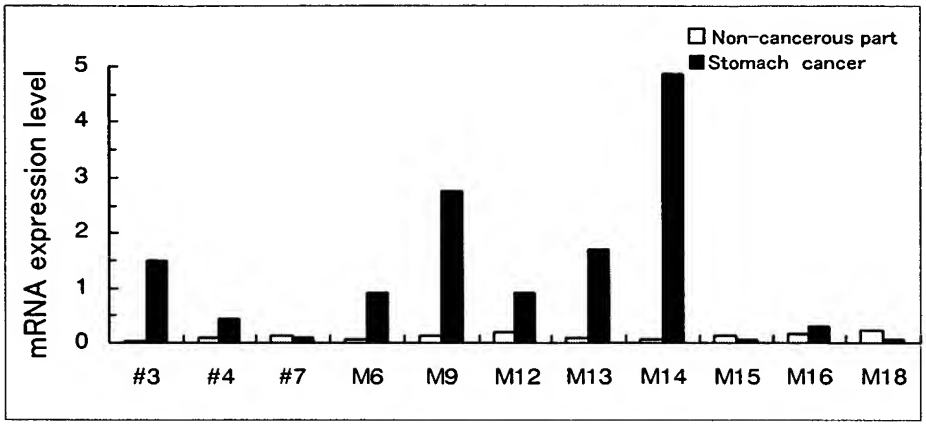

FIG. 27

TEG26

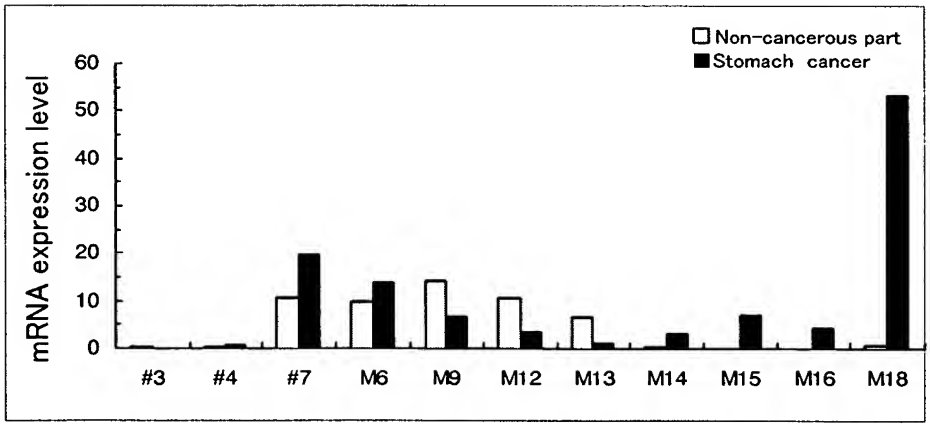

FIG. 28

TEG27

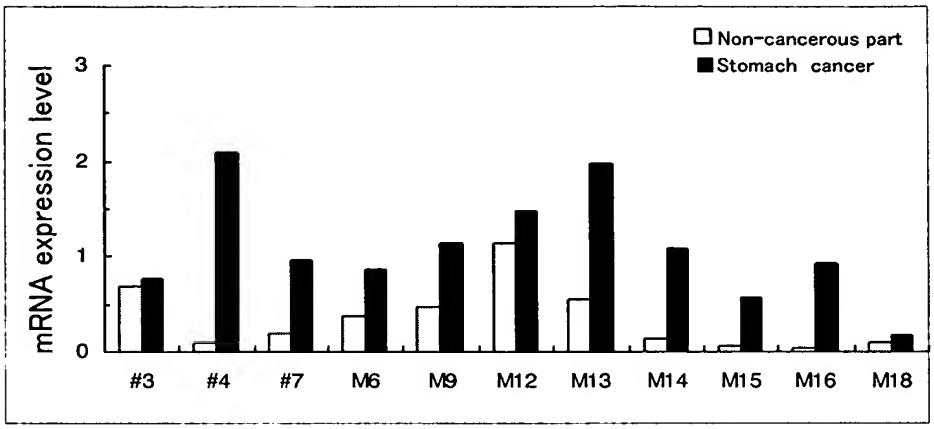

FIG. 29

TEG28

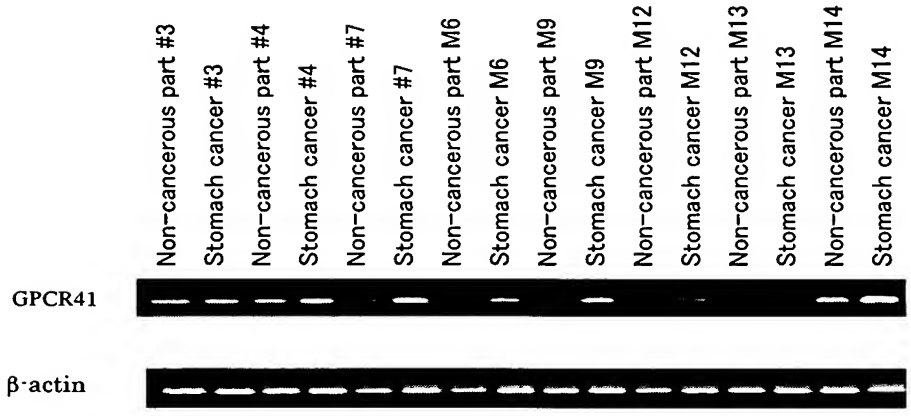

FIG. 30

TEG29

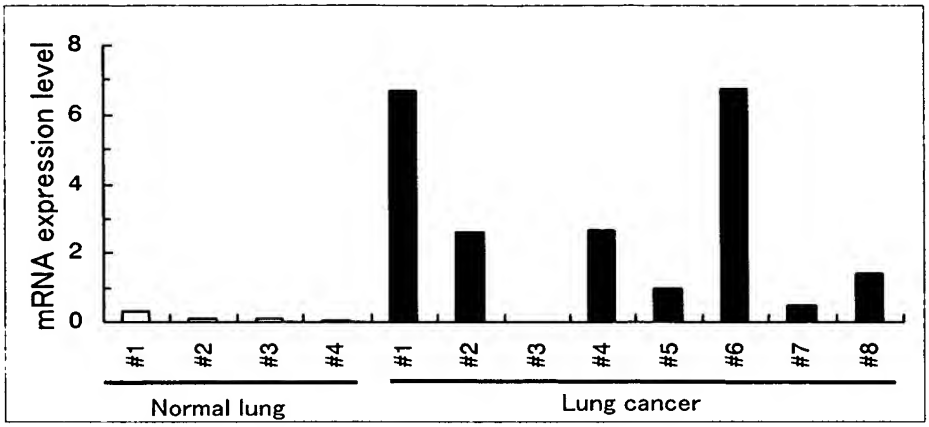

FIG. 31

TEG30

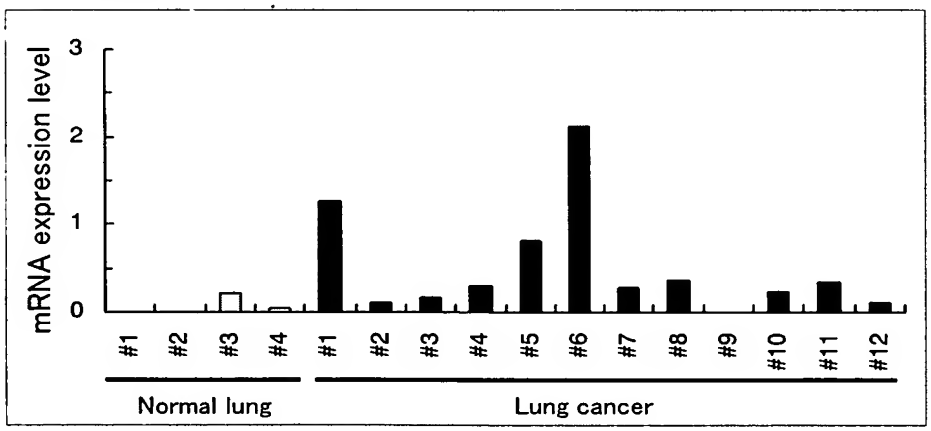

FIG. 32

TEG31

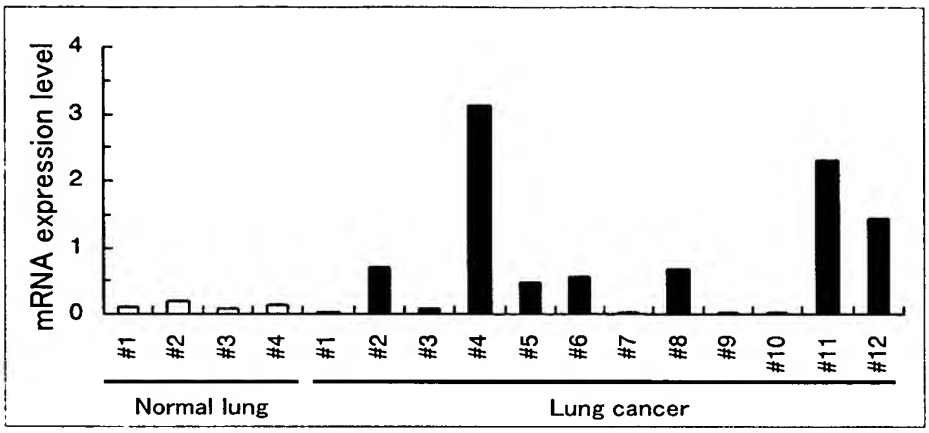

FIG. 33

TEG32

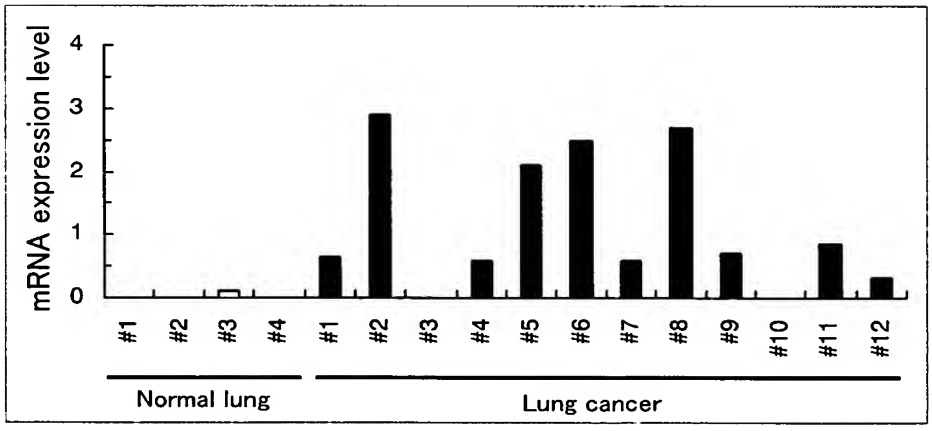

FIG. 34

TEG33

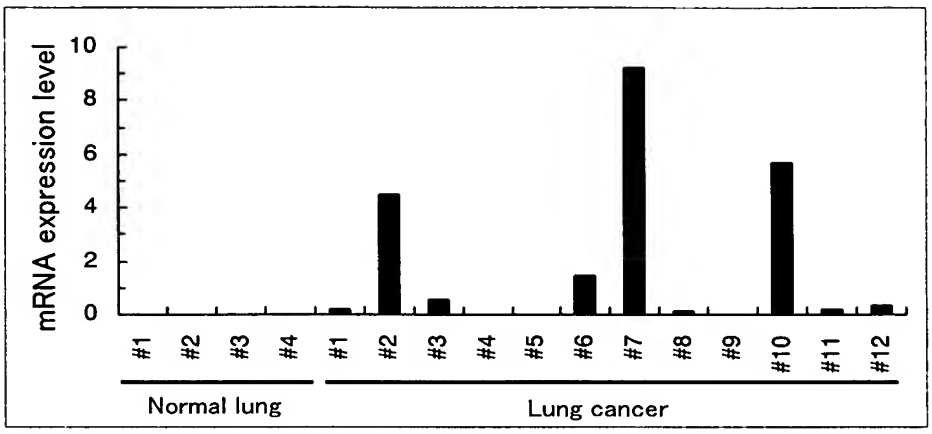

FIG. 35

TEG34

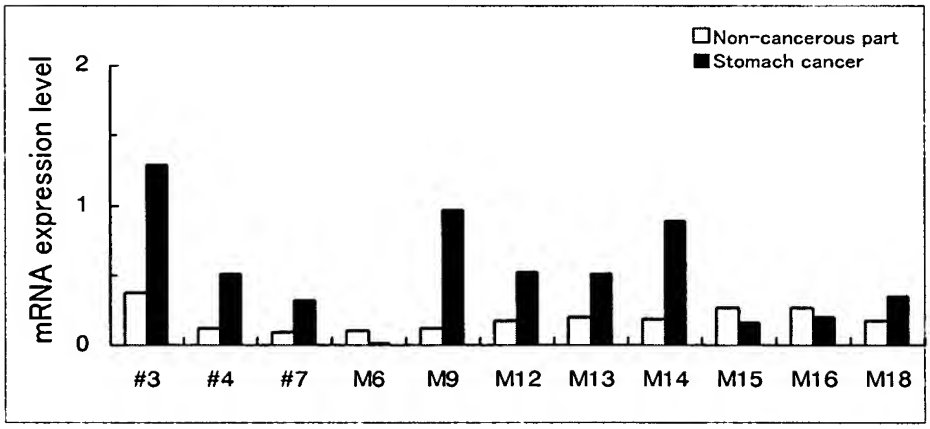

FIG. 36

TEG35

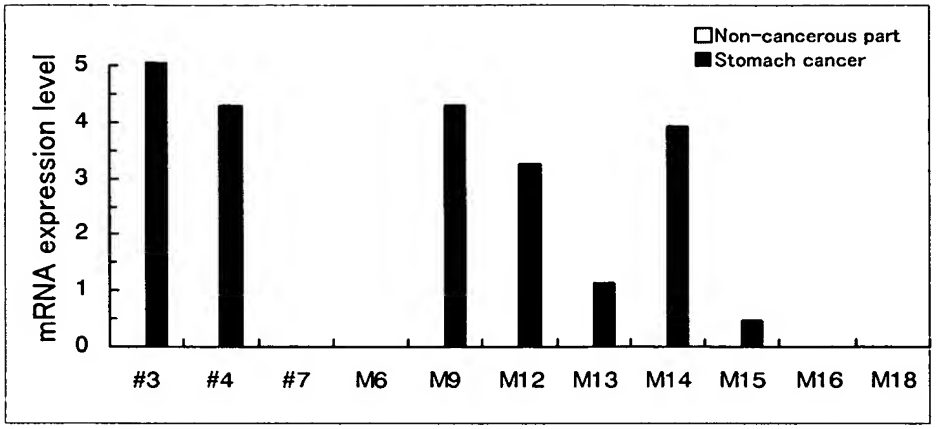

FIG. 37

TEG36

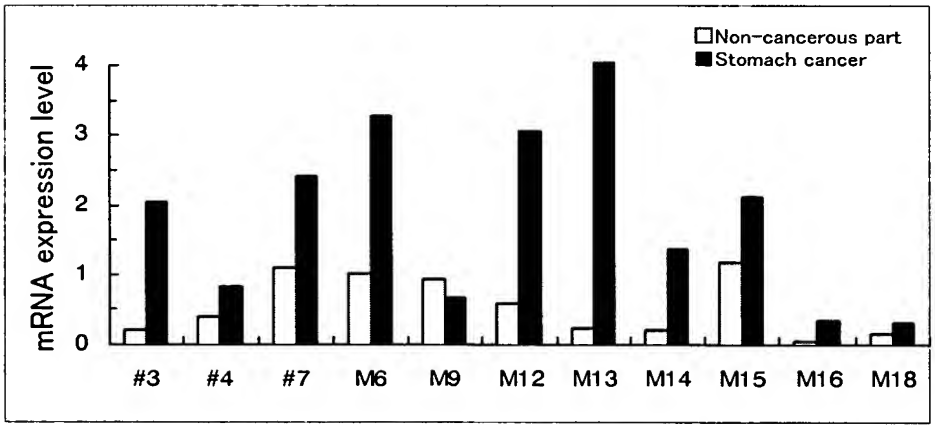

FIG. 38

TEG37

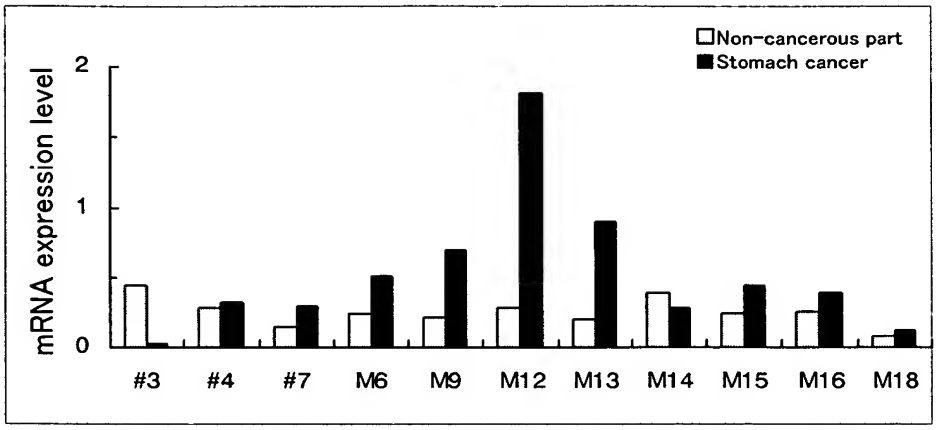

FIG. 39

TEG38

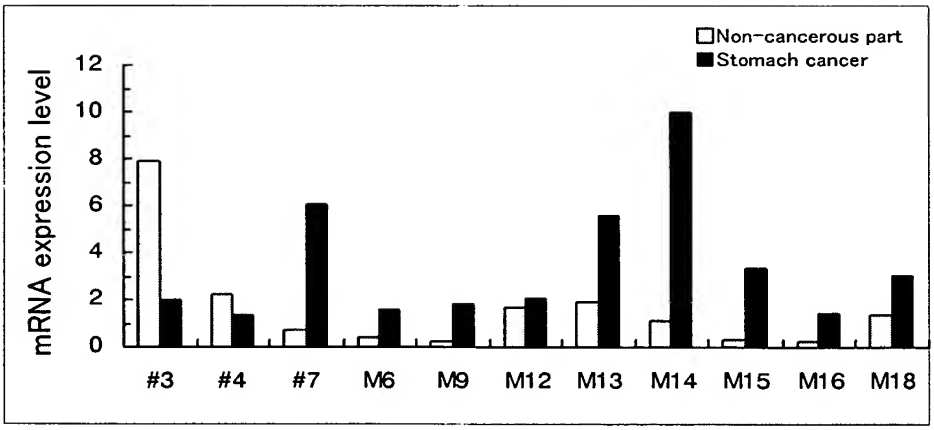

FIG. 40

TEG39

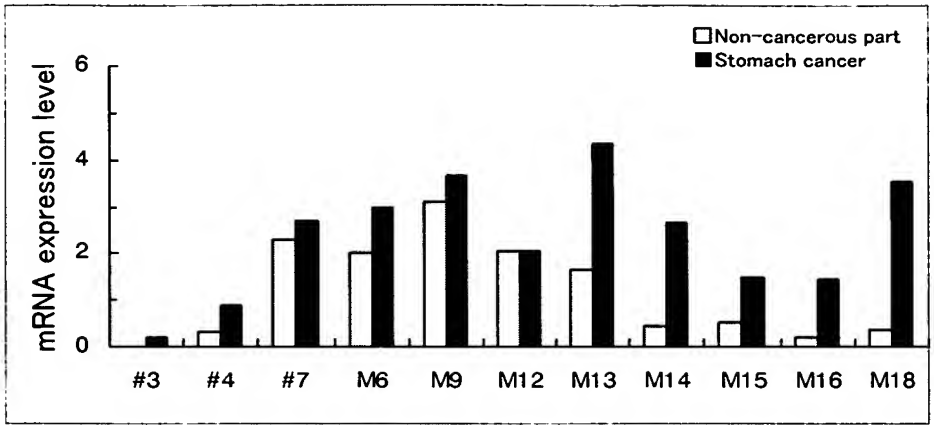

FIG. 41

TEG40

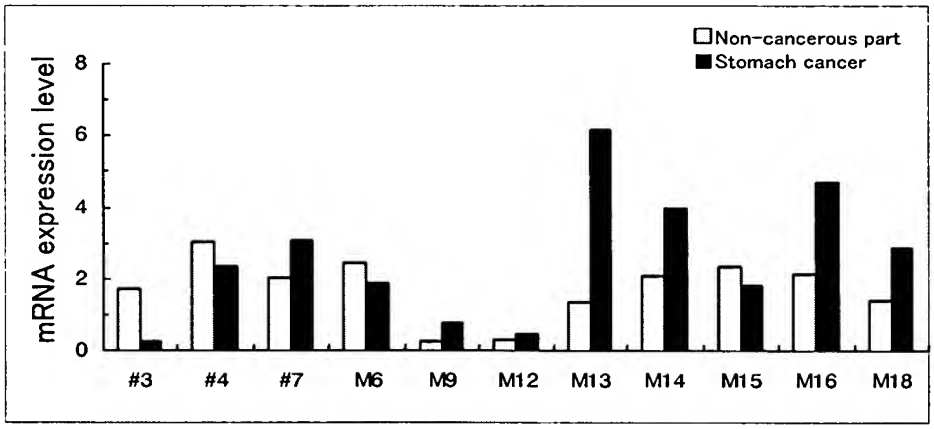

FIG. 42

TEG41

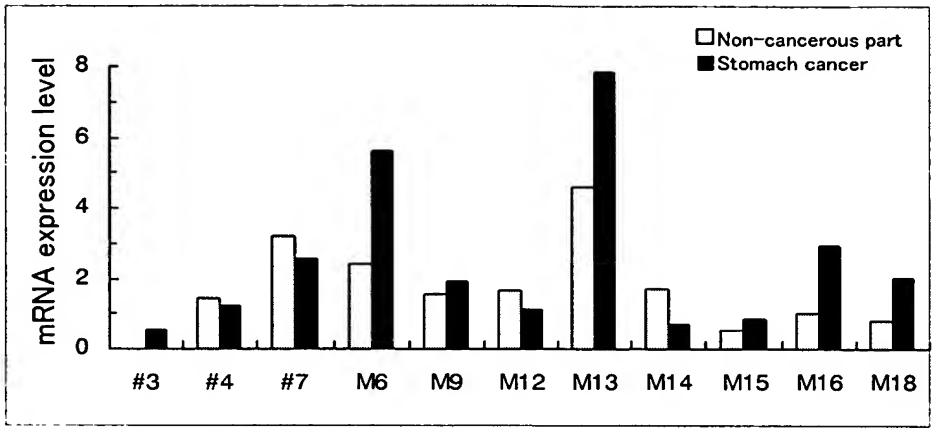

FIG. 43

TEG42

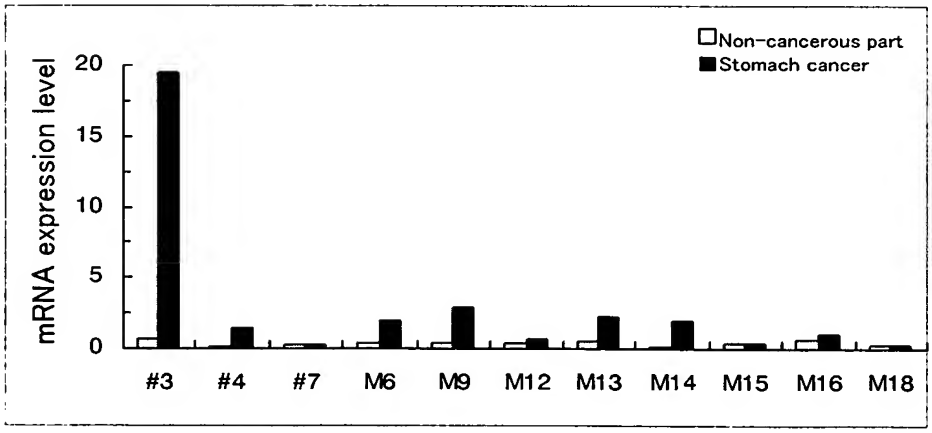

FIG. 44

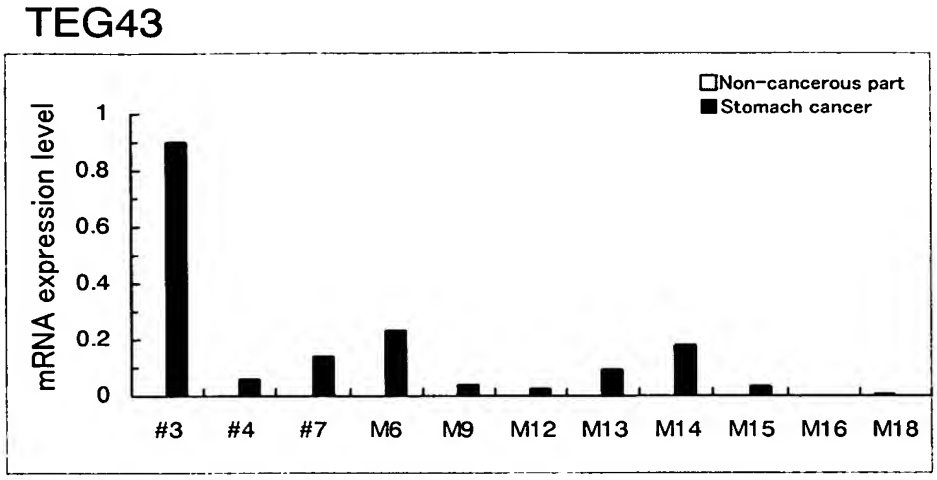
TEG43
Non-cancerous part
Stomach cancer
mRNA expression level
1
0.8
0.6
0.4
0.2
0
#3
#4
#7
M6
M9
M12
M13
M14
M15
M16
M18

FIG. 45

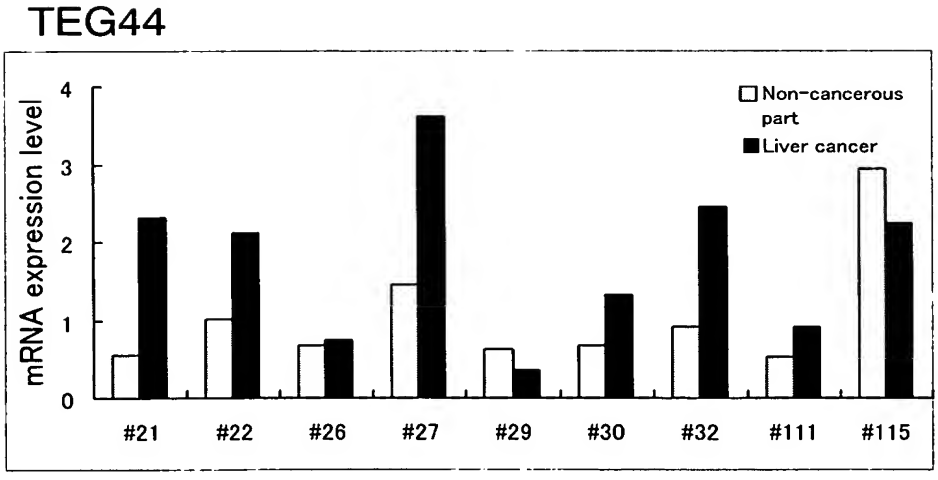
TEG44
Non-cancerous part
Liver cancer
mRNA expression level
4
3
2
1
0
#21
#22
#26
#27
#29
#30
#32
#111
#115

FIG. 46

TEG45

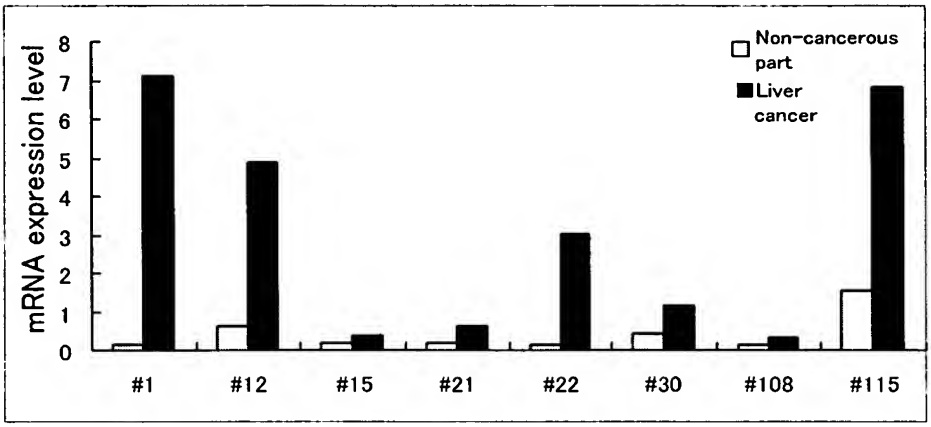

FIG. 47

TEG46

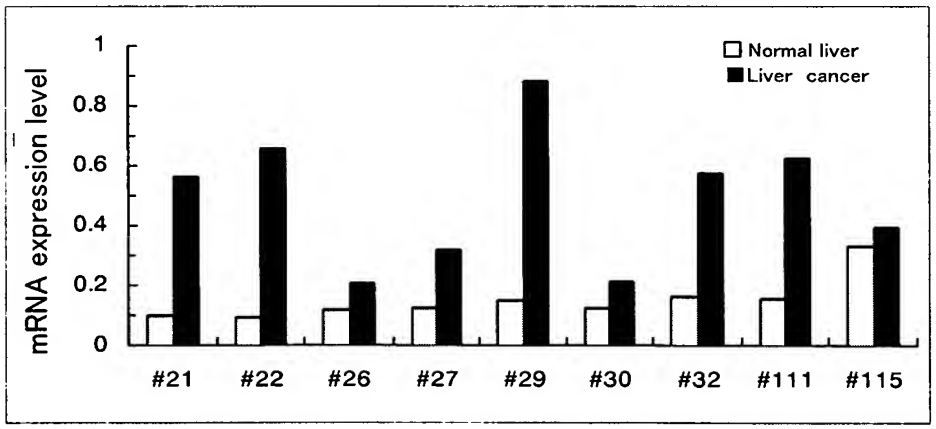

FIG. 48

TEG47

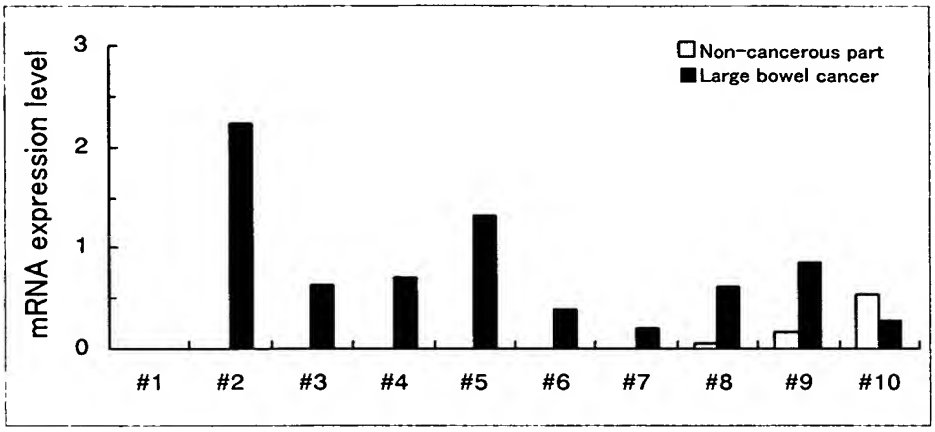

FIG. 49

TEG48

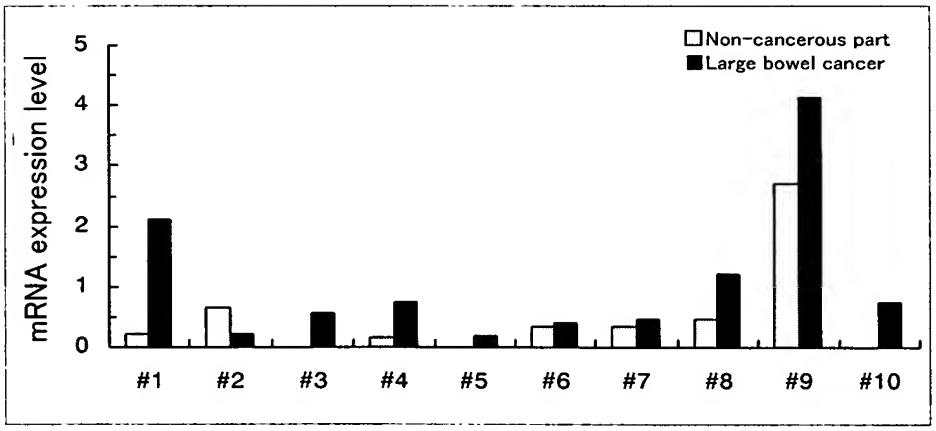

FIG. 50

TEG49

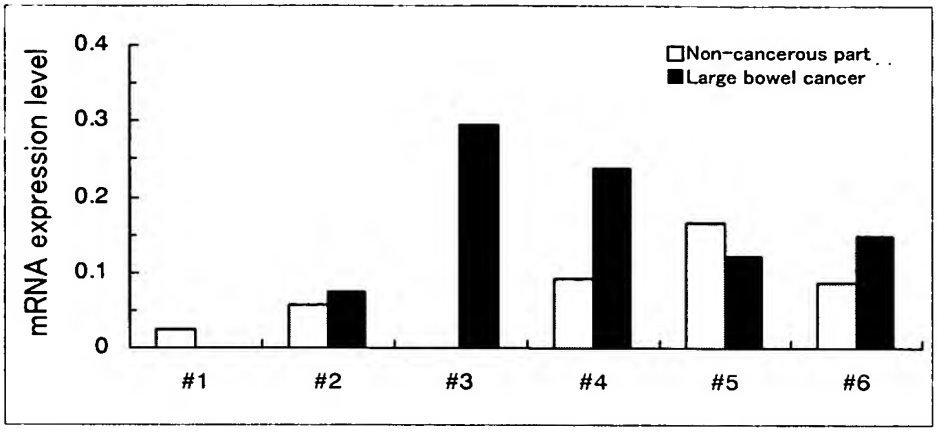

FIG. 51

TEG50

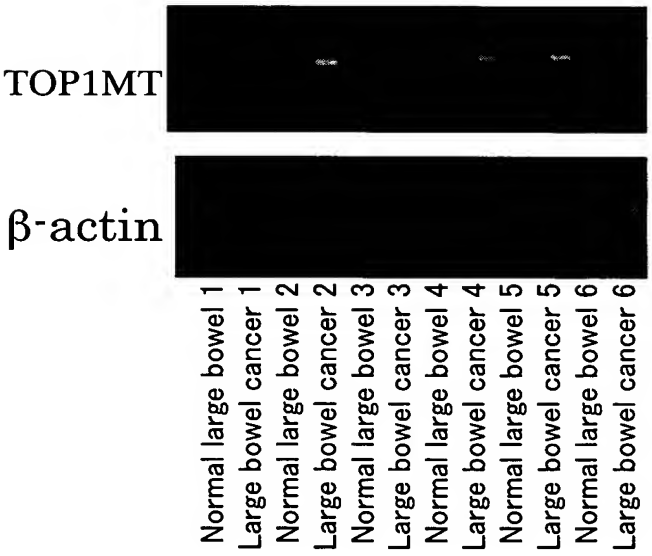

FIG. 52

TEG51

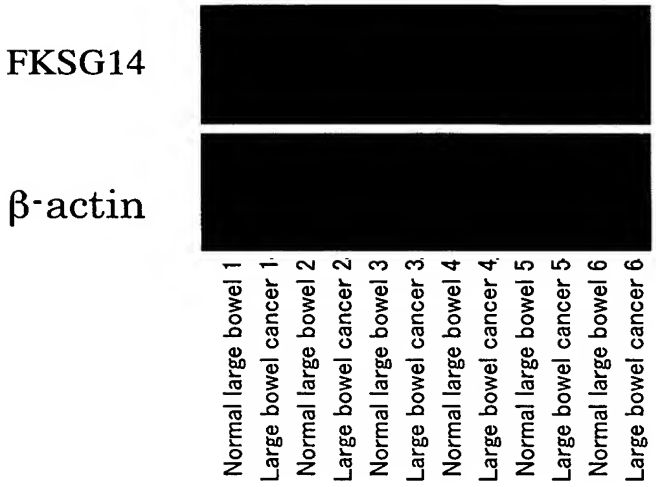

FIG. 53

TEG52

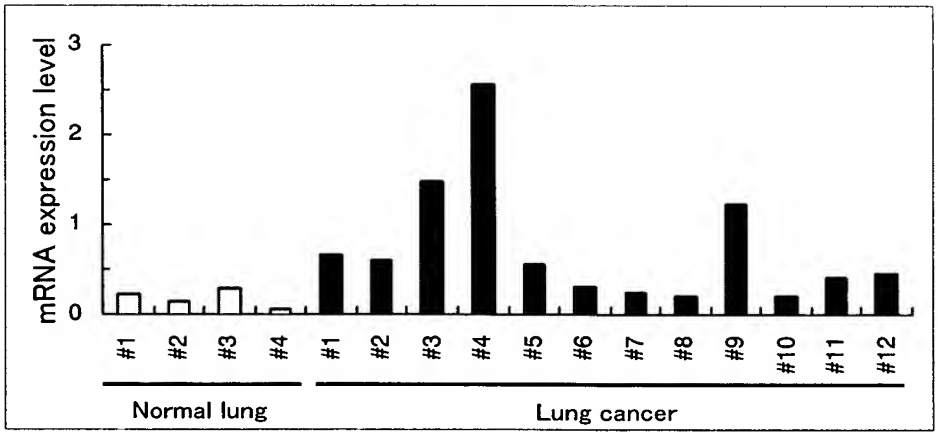

FIG. 54

TEG53

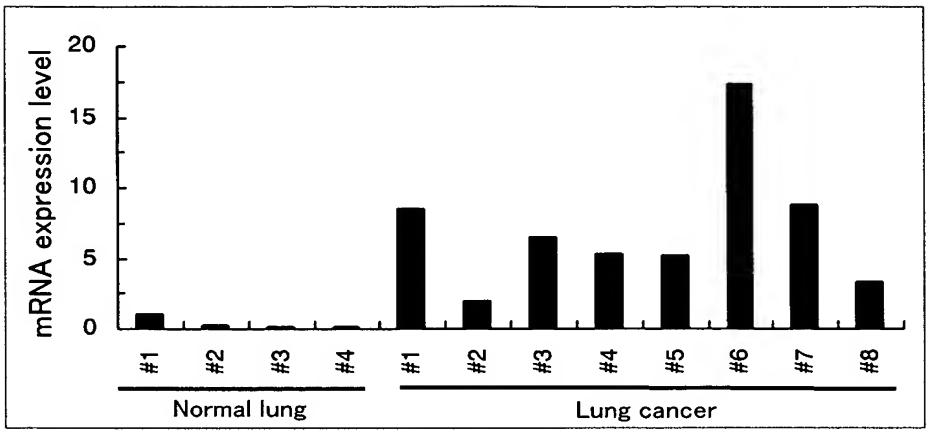

FIG. 55

TEG54

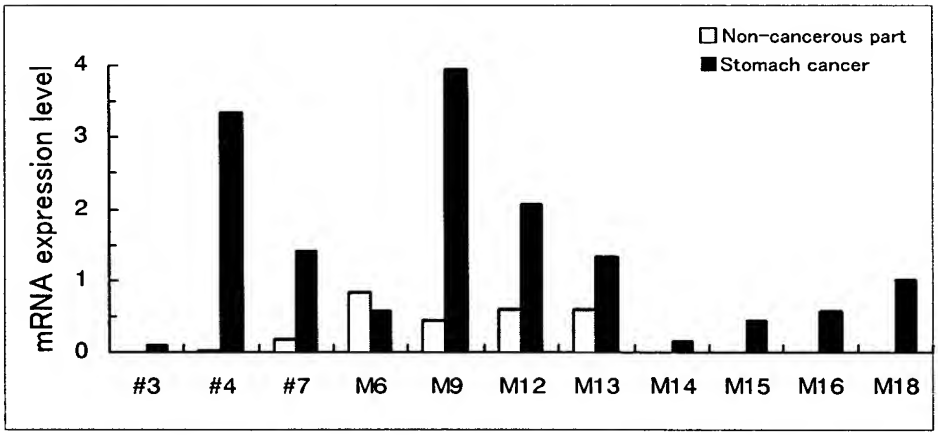

FIG. 56

TEG55

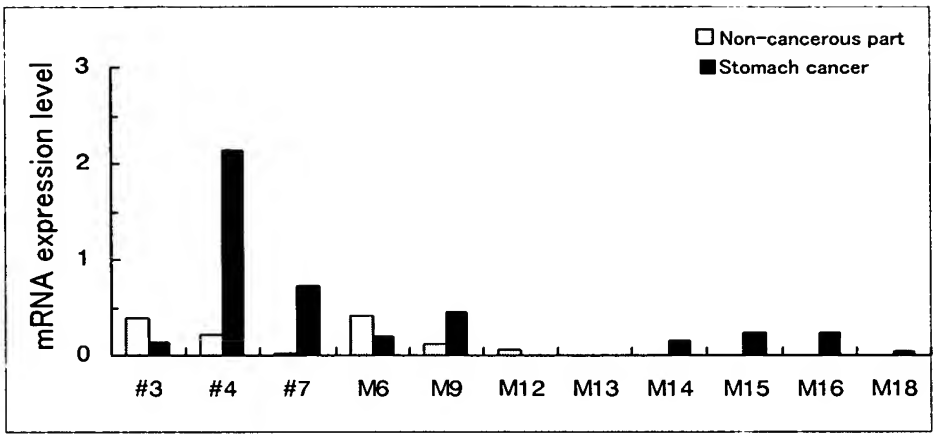

FIG. 57

TEG56

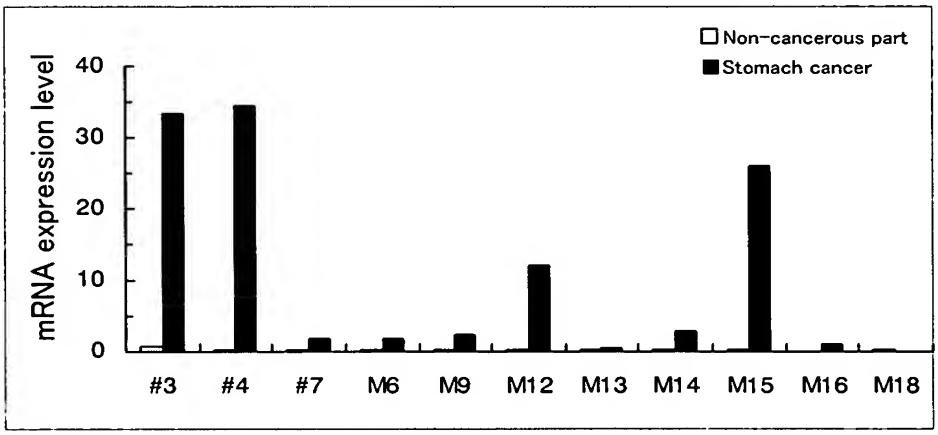

FIG. 58

TEG57

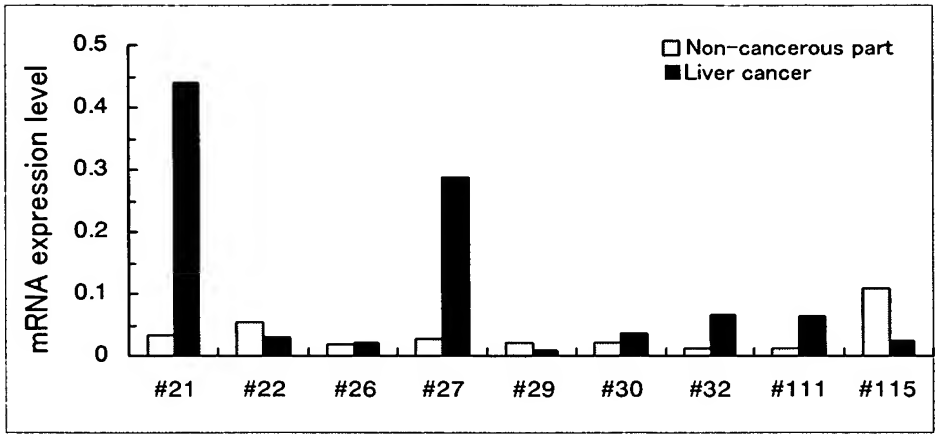

FIG. 59

TEG58

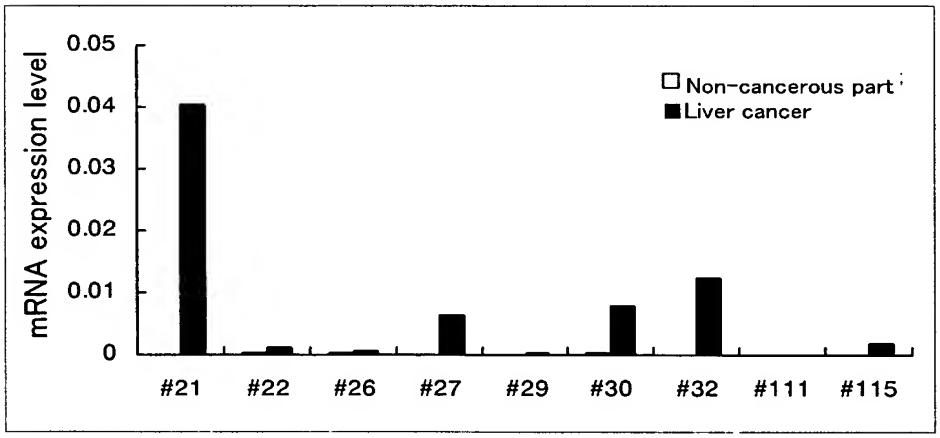

FIG. 60

TEG59

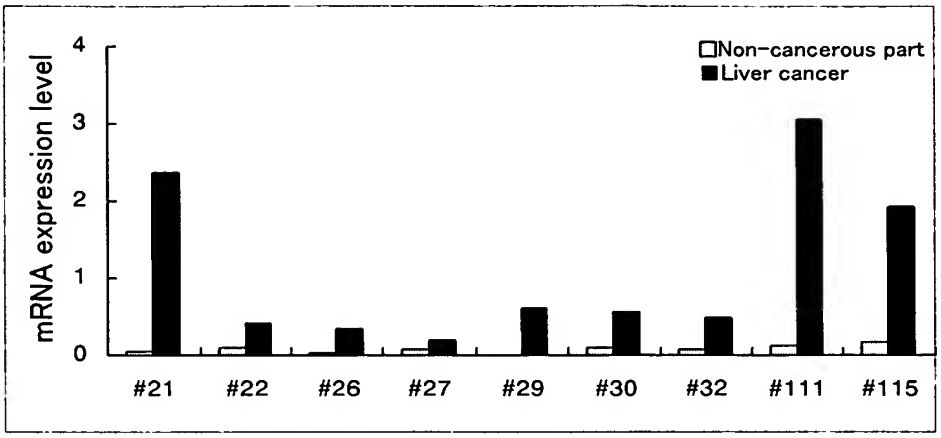

FIG. 61

TEG60

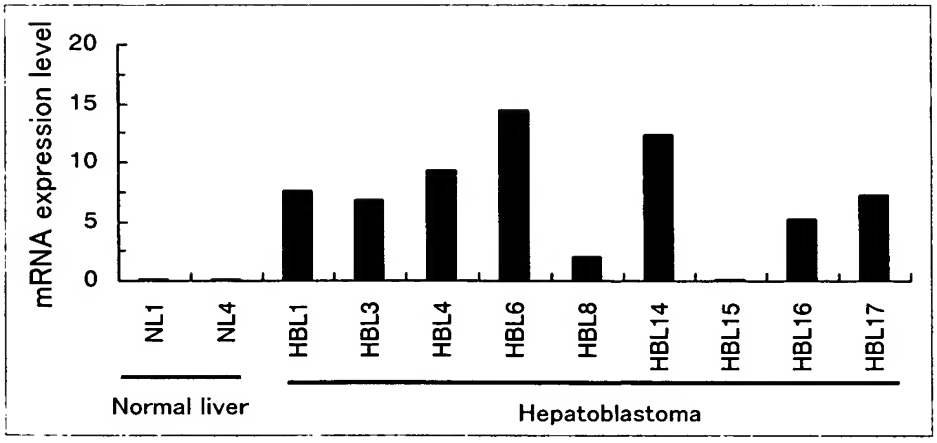

FIG. 62

TEG61

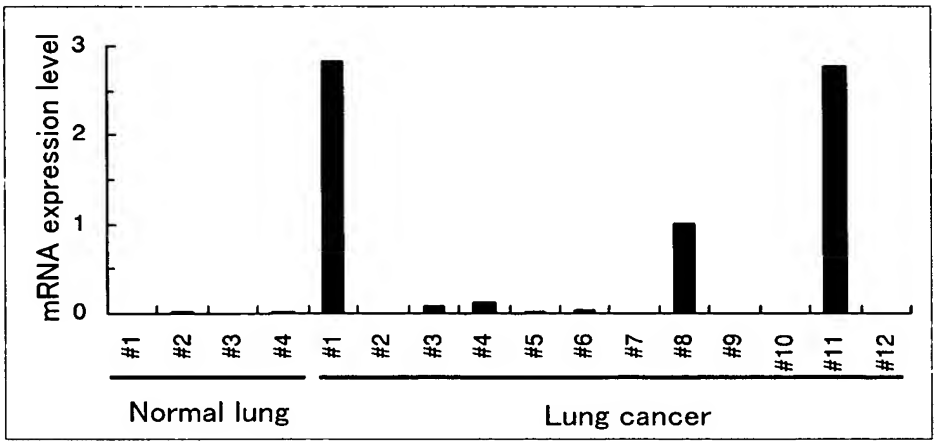

FIG. 63

TEG62

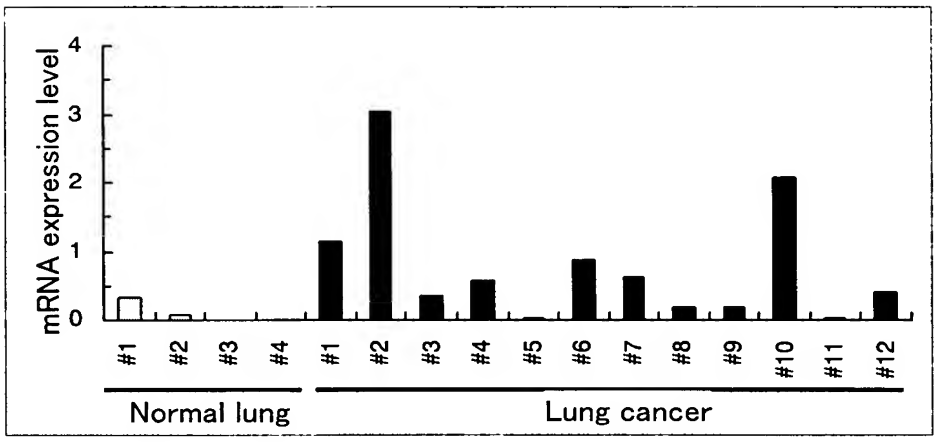

FIG. 64

TEG63

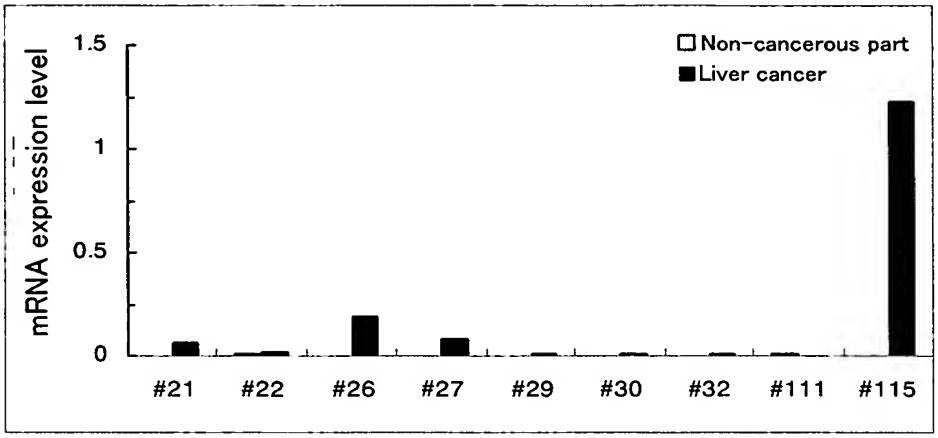

FIG. 65

TEG64

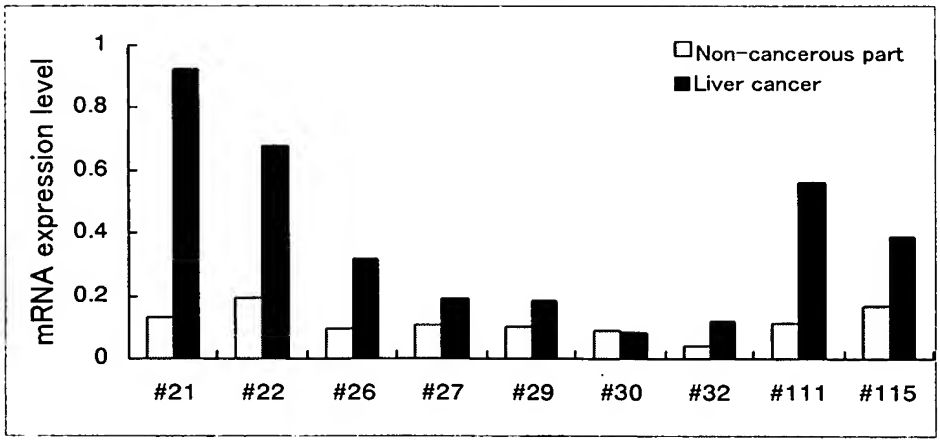

FIG. 66

```
ATGGCTTCGTTCCCCGAGACCGATTTCCAGATCTGCTTGCTGTGCAAGGAGATGTGCGGC   60
MetAlaSerPheProGluThrAspPheGlnIleCysLeuLeuCysLysGluMetCysGly   20

TCGCCGGCGCCGCTCTCCTCCAACTCGTCCGCGTCGTCGTCCTCCTCGCAGACGTCCACG  120
SerProAlaProLeuSerSerAsnSerSerAlaSerSerSerSerSerGlnThrSerThr   40

TCGTCGGGGGGCGGCGGCGGGGGCCCTGGGGCGGCGGCGCGCCGCCTACACGTCCTGCCC  180
SerSerGlyGlyGlyGlyGlyGlyProGlyAlaAlaAlaArgArgLeuHisValLeuPro   60

TGCCTGCACGCCTTCTGCCGCCCCTGCCTCGAGGCGCACCGGCTGCCGGCGGCGGGCGGC  240
CysLeuHisAlaPheCysArgProCysLeuGluAlaHisArgLeuProAlaAlaGlyGly   80

GGCGCGGCGGGAGAGCCGCTCAAGCTGCGCTGCCCCGTGTGCGACCAGAAAGTAGTGCTA  300
GlyAlaAlaGlyGluProLeuLysLeuArgCysProValCysAspGlnLysValValLeu  100

GCCGAGGCGGCGGGTATGGACGCGCTGCCTTCGTCCGCCTTCCTGCTTAACAACCTGCTC  360
AlaGluAlaAlaGlyMETAspAlaLeuProSerSerAlaPheLeuLeuAsnAsnLeuLeu  120

GACGCGGTGGTGGCCACTGCCGACGAGCCGCCGCCCAAGAACGGGCGCGCCGGCGCTCCG  420
AspAlaValValAlaThrAlaAspGluProProProLysAsnGlyArgAlaGlyAlaPro  140

GCGGGAGCGGGCGGCCACAGCAACCACCGGCACCACGCTCACCACGCGCACCCGCGCGCG  480
AlaGlyAlaGlyGlyHisSerAsnHisArgHisHisAlaHisHisAlaHisProArgAla  160

TCCGCCTCCGCGCCGCCACTCCCGCAGGCGCCGCAGCCGCCCGCGCCTTCCCGCTCGGCA  540
SerAlaSerAlaProProLeuProGlnAlaProGlnProProAlaProSerArgSerAla  180

CCCGGCGGCCCTGCCGCTTCCCCGTCGGCGCTGCTGCTCCGCCGTCCTCACGGCTGCAGC  600
ProGlyGlyProAlaAlaSerProSerAlaLeuLeuLeuArgArgProHisGlyCysSer  200

TCGTGCGATGAGGGCAACGCAGCTTCTTCGCGCTGCCTCGACTGCCAGGAGCACCTGTGC  660
SerCysAspGluGlyAsnAlaAlaSerSerArgCysLeuAspCysGlnGluHisLeuCys  220

GACAACTGCGTCCGAGCGCACCAGCGCGTGCGCCTCACCAAGGACCACTACATCGAGCGC  720
AspAsnCysValArgAlaHisGlnArgValArgLeuThrLysAspHisTyrIleGluArg  240

GGCCCGCCGGGTCCCGGTGCCGCAGCAGCGGCGCAGCAGCTCGGGCTCGGGCCGCCCTTT  780
GlyProProGlyProGlyAlaAlaAlaAlaAlaGlnGlnLeuGlyLeuGlyProProPhe  260

CCCGGCCCGCCCTTCTCCATCCTCTCAGTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCAC  840
ProGlyProProPheSerIleLeuSerValPheProGluArgLeuGlyPheCysGlnHis  280
```

FIG. 67

```
CACGACGACGAGGTGCTGCACCTGTACTGTGACACTTGCTCTGTACCCATCTGTCGTGAG  900
HisAspAspGluValLeuHisLeuTyrCysAspThrCysSerValProIleCysArgGlu  300

TGCACAATGGGCCGGCATGGGGGCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGAC  960
CysThrMetGlyArgHisGlyGlyHisSerPheIleTyrLeuGlnGluAlaLeuGlnAsp  320

TCACGGGCACTCACCATCCAGCTGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAG 1020
SerArgAlaLeuThrIleGlnLeuLeuAlaAspAlaGlnGlnGlyArgGlnAlaIleGln  340

CTGAGCATCGAGCAGGCCCAGACGGTGGCGGAACAGGTGGAGATGAAGGCGAAGGTTGTG 1080
LeuSerIleGluGlnAlaGlnThrValAlaGluGlnValGluMetLysAlaLysValVal  360

CAGTCGGAGGTCAAAGCCGTGACTGCGAGGCATAAGAAAGCCCTGGAGGAACGCGAGTGT 1140
GlnSerGluValLysAlaValThrAlaArgHisLysLysAlaLeuGluGluArgGluCys  380

GAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACCTGCAG 1200
GluLeuLeuTrpLysValGluLysIleArgGlnValLysAlaLysSerLeuTyrLeuGln  400

GTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGCAGCAG 1260
ValGluLysLeuArgGlnAsnLeuAsnLysLeuGluSerThrIleSerAlaValGlnGln  420

GTCCTGGAGGAGGGTAGAGCGCTAGACATCCTACTGGCCCGAGACCGGATGCTGGCCCAG 1320
ValLeuGluGluGlyArgAlaLeuAspIleLeuLeuAlaArgAspArgMetLeuAlaGln  440

GTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCCAGGAAGACGACCGAGTCATG 1380
ValGlnGluLeuLysThrValArgSerLeuLeuGlnProGlnGluAspAspArgValMet  460

TTCACACCCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTTGGCTTTGTTAGCAGC 1440
PheThrProProAspGlnAlaLeuTyrLeuAlaIleLysSerPheGlyPheValSerSer  480

GGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCCAGGGT 1500
GlyAlaPheAlaProLeuThrLysAlaThrGlyAspGlyLeuLysArgAlaLeuGlnGly  500

AAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCTCAGGA 1560
LysValAlaSerPheThrValIleGlyTyrAspHisAspGlyGluProArgLeuSerGly  520

GGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGCAGAGGTG 1620
GlyAspLeuMetSerAlaValValLeuGlyProAspGlyAsnLeuPheGlyAlaGluVal  540

AGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCCAGCTGGAGGGTGAGCAC 1680
SerAspGlnGlnAsnGlyThrTyrValValSerTyrArgProGlnLeuGluGlyGluHis  560
```

FIG. 67 (continued from previous page)

```
CTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGGTGGTC 1740
LeuValSerValThrLeuCysAsnGlnHisIleGluAsnSerProPheLysValValVal  580

AAGTCAGGCCGCAGCTACGTGGGCATTGGGCTCCCGGGCCTGAGCTTCGGCAGTGAGGGT 1800
LysSerGlyArgSerTyrValGlyIleGlyLeuProGlyLeuSerPheGlySerGluGly  600

GACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCTACATC 1860
AspSerAspGlyLysLeuCysArgProTrpGlyValSerValAspLysGluGlyTyrIle  620

ATTGTCGCCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCTTCCAC 1920
IleValAlaAspArgSerAsnAsnArgIleGlnValPheLysProCysGlyAlaPheHis  640

CACAAATTCGGCACCCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCGTGGCC 1980
HisLysPheGlyThrLeuGlySerArgProGlyGlnPheAspArgProAlaGlyValAla  660

TGTGACGCCTCACGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGATCTTC 2040
CysAspAlaSerArgArgIleValValAlaAspLysAspAsnHisArgIleGlnIlePhe  680

ACGTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGCAGTTC 2100
ThrPheGluGlyGlnPheLeuLeuLysPheGlyGluLysGlyThrLysAsnGlyGlnPhe  700

AACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACACGAGG 2160
AsnTyrProTrpAspValAlaValAsnSerGluGlyLysIleLeuValSerAspThrArg  720

AACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCCTAAACAAGTATGGCTTCGAG 2220
AsnHisArgIleGlnLeuPheGlyProAspGlyValPheLeuAsnLysTyrGlyPheGlu  740

GGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGGTGTGGCCTTCAACCATGAGGGCCAC 2280
GlyAlaLeuTrpLysHisPheAspSerProArgGlyValAlaPheAsnHisGluGlyHis  760

TTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTCACCCCGACTGCCAGTCG 2340
LeuValValThrAspPheAsnAsnHisArgLeuLeuValIleHisProAspCysGlnSer  780

GCACGCTTTCTGGGCTCGGAGGGCACAGGCAATGGGCAGTTCCTGCGCCCACAAGGGGTA 2400
AlaArgPheLeuGlySerGluGlyThrGlyAsnGlyGlnPheLeuArgProGlnGlyVal  800

GCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTACAGATG 2460
AlaValAspGlnGluGlyArgIleIleValAlaAspSerArgAsnHisArgValGlnMet  820

TTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTGGGCAG 2520
PheGluSerAsnGlySerPheLeuCysLysPheGlyAlaGlnGlySerGlyPheGlyGln  840
```

FIG. 67 (continued from previous page)

```
ATGGACCGCCCTTCCGGCATCGCCATCACCCCCGACGGAATGATCGTTGTGGTGGACTTT 2580
MetAspArgProSerGlyIleAlaIleThrProAspGlyMetIleValValValAspPhe  860

GGCAACAATCGAATCCTCGTCTTCTAATTGCATTTCCTAGGTTTCTGTGTTTGGGGTGTG 2640
GlyAsnAsnArgIleLeuValPhe***                                   868

TGTGCGTGTCTCTCTCTCTCTCTCTCTCTTTCTCTTTCTCTCTCTTTTTGAATTTCAAAG 2700
AAGAAACAGTCTCAGGGAAATTTCTTTTTTCTTTTTTTTTTTTTAAAGAGAACAAGAAAAG 2760
TACAACATTGCTTAAGTCCTACCTCATCTTTATTTTTTTACAGATGAATGTACTTATCTT 2820
TTCTGCAGGGATTGAGCCTGTGAAGTGATAATTTCTATCTACCTCATAAATCTTTACATT 2880
TCCTTCTGCAACAGGCCCTCTTCCCCTCCTCAGTGGAGTTTGCATTTCCCTCTTCCCCTG 2940
CGTGGGGCATGATATGCACAAGCCTGGCATCTGTATGGCTGGGAGGGCACTGGATGTGTG 3000
TGGTGGGGTGTATTCTGTAGATTGAGCCAAGGAAACACAAAAAAAAACTACTAAGTAAAA 3060
AAACAAAAAACTATAAAACATGGAAAAAATAGGATTTGAAATGCATAATTATAGAATACC 3120
TGTGTTCTTGAGAATACTGTTTATATGGGGTTTAGATTATGTTGTGTTGTTTTGATCTTT 3180
TTGGAAAATCTTCTCTTTTTAAATGCTGCAACAGAGAAATTTCCTCTGTTCTCTGTTTAT 3240
ACCTCTTAATTGTATTGTCCAAGGCAGACATGATATAAGGAATATGCACTACCGTAGTAA 3300
CTCCCCTGGCCGCAGAAACCACACTGCAAGCCTGTCCGGGGTGGGGTGCTGACTGCCATT 3360
TGCCACTTTTAAATGGGCACTGCCGTGGTAATGTGAATCCC                     3401
```

FIG. 67 (continued from previous page)

```
K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc    1:ATGCGCGGACTGACCCAGCGGCCGGCGCGGCGGCGCCGGGCGGACTTAATCGCGGGCGCA 60

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc   61:GCGCGAGGCTCGGGACCCAGAGCACCACCTACCGGCGGCACGGTCGGCGCAGCAGGCCCC 120

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc  121:AGAAGGGCGGGGAACGCTGTCAAGCCCAGGGGCACTTCGGCGAGGAGCCCCACCCGCCCT 180

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc  181:CCAGCTGACCCTCAGCTGTGGCCCACATCCGGGGCCCAGAGCGCCGCGGAAACGCCGAAG 240

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc  241:CCCGGCCGGCAGATAGCGCGGAAAGCGAAGAAGGAAGTTCCCGTCCCTCCTAAAGCCGAA 300

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc  301:GCCAAAGCGAAGTCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCGCAGCCACAAA 360

K#1.nuc          1:------------------------------------------------------------ 1
XM_067369.nuc  361:AAAAAGAAGATCCGCACGTCACCCACCTTACGGCGGCCCAAGACACCGCGACTCCGGAGA 420

K#1.nuc          1:------------CCCTCCTCCGGGCTGGGTTGCAAATGGCTTCGTTCCCCGAGACCGATT 48
                               * ***    * **    *   *   *    **  **   *     *
XM_067369.nuc  421:CAGCCCAAATATC-CTCGGAAGAGCGCTCCTAGGAGAAACAAGCTTGACCACTATGCTAT 479

K#1.nuc         49:TCCAGATCTGCTTGCTGTGCAAGGAGATGTGCGGCTCGCCGGCGCCGCTCTCCTCCAACT 108
                     *  * **    *  **  ***     *     *  *        *     **
XM_067369.nuc  480:CATCAAGTTTCTGCT-GACCACTGAGTCTGCCATGAAGAAGATAGAAGACAATAACACAC 538

K#1.nuc        109:C-GTCCGCGTCGTCGTCCTCCTCGCAGACGTCCACGTCGTCGGGGGGCGGCGGCGGGGGC 167
                    **   * * ** *   *    **  **   ***    *      *     *  *  **
XM_067369.nuc  539:TTGTGTTCATTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGC 598

K#1.nuc        168:CCTGGGGCGGCGGCGCGCCGCCTACACGTCCTGCCCTGCCTGCACGCCTTCTGCCGCCCC 227
                    **  * *   *  * *            *     * *   *         *  *
XM_067369.nuc  599:TCTATGACAAAGATGTGGTCAAGGTCAACACCCTGATTCGGCCTGATGGAGAGAAGAAGG 658

K#1.nuc        228:TGCCTCGAGGCGCACCGGCTGCCGGCGGCGGGCGGCGGCGCGGCGGGAGAGCCGCTCAAG 287
                    *** *      *  ** ** ** **   *  *   *  **   *     ** *    *
XM_067369.nuc  659:CGCCGCAGCCGCCCGCGCCTTCCCGCTCGGCACCCGGCGGCCCTGCCGCTTCCCCGTCGG 718
```

FIG. 68

```
K#1.nuc          288:CTGCGCTGCCCCGTGTGCGACCAGAAAGTAGTGCTAGCCGAGGCGGCGGGTATGGACGCG 347
                     *   ***** ***    *  *  *   * **  *  **   *  ***      *
XM_067369.nuc    719:CGCTGCTGCTCCGCCGTCCTCACGGCTGCAGCTCGTGCGATGAGGGCAACGCAGCTTCTT 778

K#1.nuc          348:CTGCCTTCGTCCGCCTTCCTGCTTAACAACCTGCTCGACGCGGTGGTGGCCACTGCCGAC 407
                     *   ** * **  *   *  *   * *     *      ***   * *  ***   **
XM_067369.nuc    779:CGCGCTGCCTCGACTGCCAGGAGCACCTGTGCGACAACTGCGTCCGAGCGCACCAGCGCG 838

K#1.nuc          408:GAGCCGCCGCCCAAGAACGGGCGCGCCGGCGCTCCGGCGGGAGCGGGCGGCCAC-AGCAA 466
                       *  * ** * ** *       *  ****  *     * *     *  *   ****
XM_067369.nuc    839:TGCGCCTCACCAAGGACCACTACATCGAGCGCGGCCCGCCGGGTCCCGGTGCCGCAGCAG 898

K#1.nuc          467:CCACCGGCACCACGCTCACCACGCGCACCCGCGCGCGTCCGCCTCCGCGCCGCCACTCCC 526
                     *  *     *  * *   *   *  * ***   * ** **  * *  * **  *    *
XM_067369.nuc    899:CGGCGCAG-CAGCTCGGGCTCGGGCCGCCCTTTCCCGGCCCGCCCTTCTCCATCCTCTCA 957

K#1.nuc          527:GCAGGCGCCGCAGCCGCCCGCGCCTTCCCGCTCGGCACCCGGCGGCCCTGCCGCTTCCCC 586
                     *      ***    *  * **  ** ** ** *  *  *     *    * *  *** *
XM_067369.nuc    958:GTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCACCACGACGACGAGTTGGGGCTTTTCACT 1017

K#1.nuc          587:GTCGGCGCTGCTGCTCCGCCGTCCTCACGGCTGCAGCTCGTGCGATGAGGGCAACGCAG- 645
                        *   ** *   * *       *          ****        *  *  * *
XM_067369.nuc   1018:AGTTCTGTGCCTCCAGAGTCCGAAAGGCCTGCAGGCTCCGTGGCCCAGCCGGCATCCGGG 1077

K#1.nuc          646:CTTCTTCGCGCTGCCTCGACTGCCAGGAGCACCTGTGCGACAACTGCGTCCGAGCGCACC 705
                     *       *   * *  *    **  *  * **    *   *** **   *    *  **
XM_067369.nuc   1078:CGGGGAATCCAAGGCGAGGAATCCGAGGTCGCCGTCCCCGGAACAGCTGGCCGCGGGCCC 1137

K#1.nuc          706:AGCGCGTGCGCCTCACCAAGGACCACTACATCGAGCGCGGCCCGCCGGGTCCCGGTGCCG 765
                       ******  *    *  **   *      **   **
XM_067369.nuc   1138:GCTGCGTGCCGCGGGTCCCGGGAGAGGCGGGCGCAGGCTAGAGCAGCAAAGGAAACTTTT 1197

K#1.nuc          766:CAGCAGCGGCGCAGCAGCTCGGGCTCGGGCCGCCCTTTCCCGGCCCGCCCTTCTCCATCC 825
                     * *   *       ** *  ** * *      *    *      *      *   ** *
XM_067369.nuc   1198:CTGGTACATTCTTACATCCAGGCCACTAATATCAGACTAGGTAACACAGTCTTAACAACT 1257

K#1.nuc          826:TCTCAGTGTTTCCCGAGCGCCTCGGCTTCTGCCAGCACCACGACGACGAGGTGCTGCACC 885
                     * ** *  *                              * *      *  *   *********
XM_067369.nuc   1258:TTTCTGGATAATGAAGCTAAGATTCAGGGCAAACTCTCATGCCAGGAGG--TGCTGCACC 1315
```

FIG. 68 (continued from previous page)

```
K#1.nuc          886:TGTACTGTGACACTTGCTCTGTACCCATCTGTCGTGAGTGCACAATGGGCCGGCATGGGG 945
                     ************************************************************
XM_067369.nuc   1316:TGTACTGTGACACTTGCTCTGTACCCATCTGTCGTGAGTGCACAATGGGCCGGCATGGGG 1375

K#1.nuc          946:GCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGACTCACGGGCACTCACCATCCAGC 1005
                     ************************************************************
XM_067369.nuc   1376:GCCACAGCTTCATCTACCTCCAGGAGGCACTGCAGGACTCACGGGCACTCACCATCCAGC 1435

K#1.nuc         1006:TGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAGCTGA---------------------- 1047
                     ************************************    *
XM_067369.nuc   1436:TGCTGGCAGATGCCCAGCAGGGACGACAGGCAATCCAGACAAAGCAGAAGAAGCTGCTTC 1495

K#1.nuc         1048:----------GCATCGAGCAGGCCCAGACGGTGGCGGAACAGGTGGAGATGAAGGCGAAGG 1098
                           ***************************************************
XM_067369.nuc   1496:TGCAGCTGAGCATCGAGCAGGCCCAGACGGTGGCGGAACAGGTGGAGATGAAGGCGAAGG 1555

K#1.nuc         1099:TTGTGCAGTCGGAGGTCAAAGCCGTGACTGCGAGGCATAAGAAAGCCCTGGAGGAACGCG 1158
                     ***************************** ********************************
XM_067369.nuc   1556:TTGTGCAGTCGGAGGTCAAAGCCGTGACGGCGAGGCATAAGAAAGCCCTGGAGGAACGCG 1615

K#1.nuc         1159:AGTGTGAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACC 1218
                     ************************************************************
XM_067369.nuc   1616:AGTGTGAGCTGCTGTGGAAGGTAGAAAAGATCCGCCAGGTGAAAGCCAAGTCTCTGTACC 1675

K#1.nuc         1219:TGCAGGTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGC 1278
                     ************************************************************
XM_067369.nuc   1676:TGCAGGTGGAGAAGCTGCGGCAAAACCTCAACAAGCTTGAGAGCACCATCAGTGCCGTGC 1735

K#1.nuc         1279:AGCAGGTCCTGGAGGAGGGTAGAGCGCTAGACATCCTACTGGCCCGAGACCGGATGCTGG 1338
                     ************************************************************
XM_067369.nuc   1736:AGCAGGTCCTGGAGGAGGGTAGAGCGCTAGACATCCTACTGGCCCGAGACCGGATGCTGG 1795

K#1.nuc         1339:CCCAGGTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCCAGGAAGACGACCGAG 1398
                     ************************************************************
XM_067369.nuc   1796:CCCAGGTGCAGGAGCTGAAGACCGTGCGGAGCCTCCTGCAGCCCCAGGAAGACGACCGAG 1855

K#1.nuc         1399:TCATGTTCACACCCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTTGGCTTTGTTA 1458
                     ************************************************************
XM_067369.nuc   1856:TCATGTTCACACCCCCCGATCAGGCACTGTACCTTGCCATCAAGTCTTTTGGCTTTGTTA 1915
```

FIG. 68 (continued from previous page)

```
K#1.nuc         1459:GCAGCGGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCC 1518
                     ************************************************************
XM_067369.nuc   1916:GCAGCGGGGCCTTTGCCCCACTCACCAAGGCCACAGGCGATGGCCTCAAGCGTGCCCTCC 1975

K#1.nuc         1519:AGGGTAAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCT 1578
                     ************************************************************
XM_067369.nuc   1976:AGGGTAAGGTGGCCTCCTTCACAGTCATTGGTTATGACCACGATGGTGAGCCCCGCCTCT 2035

K#1.nuc         1579:CAGGAGGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGCAG 1638
                     ************************************************************
XM_067369.nuc   2036:CAGGAGGCGACCTGATGTCGGCTGTGGTCCTGGGCCCTGATGGCAACCTGTTTGGTGCAG 2095

K#1.nuc         1639:AGGTGAGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCCAGCTGGAGGGTG 1698
                     ************************************************************
XM_067369.nuc   2096:AGGTGAGTGATCAGCAGAATGGGACATACGTGGTGAGTTACCGACCCCAGCTGGAGGGTG 2155

K#1.nuc         1699:AGCACCTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGG 1758
                     ************************************************************
XM_067369.nuc   2156:AGCACCTGGTATCTGTGACACTGTGCAACCAGCACATTGAGAACAGCCCTTTCAAGGTGG 2215

K#1.nuc         1759:TGGTCAAGTCAGGCCGCAGCTACGTGGGCATTGGGCTCCCGGGCCTGAGCTTCGGCAGTG 1818
                     ************************************************************
XM_067369.nuc   2216:TGGTCAAGTCAGGCCGCAGCTACGTGGGCATTGGGCTCCCGGGCCTGAGCTTCGGCAGTG 2275

K#1.nuc         1819:AGGGTGACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCT 1878
                     ************************************************************
XM_067369.nuc   2276:AGGGTGACAGCGATGGCAAGCTCTGCCGCCCTTGGGGTGTGAGTGTAGACAAGGAGGGCT 2335

K#1.nuc         1879:ACATCATTGTCGCCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCT 1938
                     ************************************************************
XM_067369.nuc   2336:ACATCATTGTCGCCGACCGCAGCAACAACCGCATCCAGGTGTTCAAGCCCTGCGGCGCCT 2395

K#1.nuc         1939:TCCACCACAAATTCGGCACCCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCG 1998
                     ************************************************************
XM_067369.nuc   2396:TCCACCACAAATTCGGCACCCTGGGCTCCCGGCCTGGGCAGTTCGACCGACCAGCCGGCG 2455

K#1.nuc         1999:TGGCCTGTGACGCCTCACGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGA 2058
                     ************************************************************
XM_067369.nuc   2456:TGGCCTGTGACGCCTCACGCAGGATCGTGGTGGCTGACAAGGACAATCATCGCATCCAGA 2515
```

FIG. 68 (continued from previous page)

```
K#1.nuc         2059:TCTTCACGTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGC 2118
                     ************************************************************
XM_067369.nuc   2516:TCTTCACGTTCGAGGGCCAGTTCCTCCTCAAGTTTGGTGAGAAAGGAACCAAGAATGGGC 2575

K#1.nuc         2119:AGTTCAACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACA 2178
                     ************************************************************
XM_067369.nuc   2576:AGTTCAACTACCCTTGGGATGTGGCGGTGAATTCTGAGGGCAAGATCCTGGTCTCAGACA 2635

K#1.nuc         2179:CGAGGAACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCCTAAACAAGTATGGCT 2238
                     ************************************************************
XM_067369.nuc   2636:CGAGGAACCACCGGATCCAGCTGTTTGGGCCTGATGGTGTCTTCCTAAACAAGTATGGCT 2695

K#1.nuc         2239:TCGAGGGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGGTGTGGCCTTCAACCATGAGG 2298
                     ************************************************************
XM_067369.nuc   2696:TCGAGGGGGCTCTCTGGAAGCACTTTGACTCCCCACGGGGTGTGGCCTTCAACCATGAGG 2755

K#1.nuc         2299:GCCACTTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTCACCCCGACTGCC 2358
                     ************************************************************
XM_067369.nuc   2756:GCCACTTGGTGGTCACTGACTTCAACAACCACCGGCTCCTGGTTATTCACCCCGACTGCC 2815

K#1.nuc         2359:AGTCGGCACGCTTTCTGGGCTCGGAGGGCACAGGCAATGGGCAGTTCCTGCGCCCACAAG 2418
                     ************************************************************
XM_067369.nuc   2816:AGTCGGCACGCTTTCTGGGCTCGGAGGGCACAGGCAATGGGCAGTTCCTGCGCCCACAAG 2875

K#1.nuc         2419:GGGTAGCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTAC 2478
                     ************************************************************
XM_067369.nuc   2876:GGGTAGCTGTGGACCAGGAAGGGCGCATCATTGTGGCGGATTCCAGGAACCATCGGGTAC 2935

K#1.nuc         2479:AGATGTTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTG 2538
                     ************************************************************
XM_067369.nuc   2936:AGATGTTTGAATCCAACGGCAGCTTCCTGTGCAAGTTTGGTGCTCAAGGCAGCGGCTTTG 2995

K#1.nuc         2539:GGCAGATGGACCGCCCTTCCGGCATCGCCATCACCCCCGACGGAATGATCGTTGTGGTGG 2598
                     ************************************************************
XM_067369.nuc   2996:GGCAGATGGACCGCCCTTCCGGCATCGCCATCACCCCCGACGGAATGATCGTTGTGGTGG 3055

K#1.nuc         2599:ACTTTGGCAACAATCGAATCCTCGTCTTCTAATTGCATTTCCTAGGTTTCTGTGTTTGGG 2658
                     ********************************
XM_067369.nuc   3056:ACTTTGGCAACAATCGAATCCTCGTCTTCTAA---------------------------- 3087

K#1.nuc         2659:GTGTGTGTGCGTGTCTCTCTCTCTCTCTCTCTCTTTCTCTTTCTCTCTCTTTTTGAATTT 2718
XM_067369.nuc   3088:------------------------------------------------------------ 3088
```

FIG. 68 (continued from previous page)

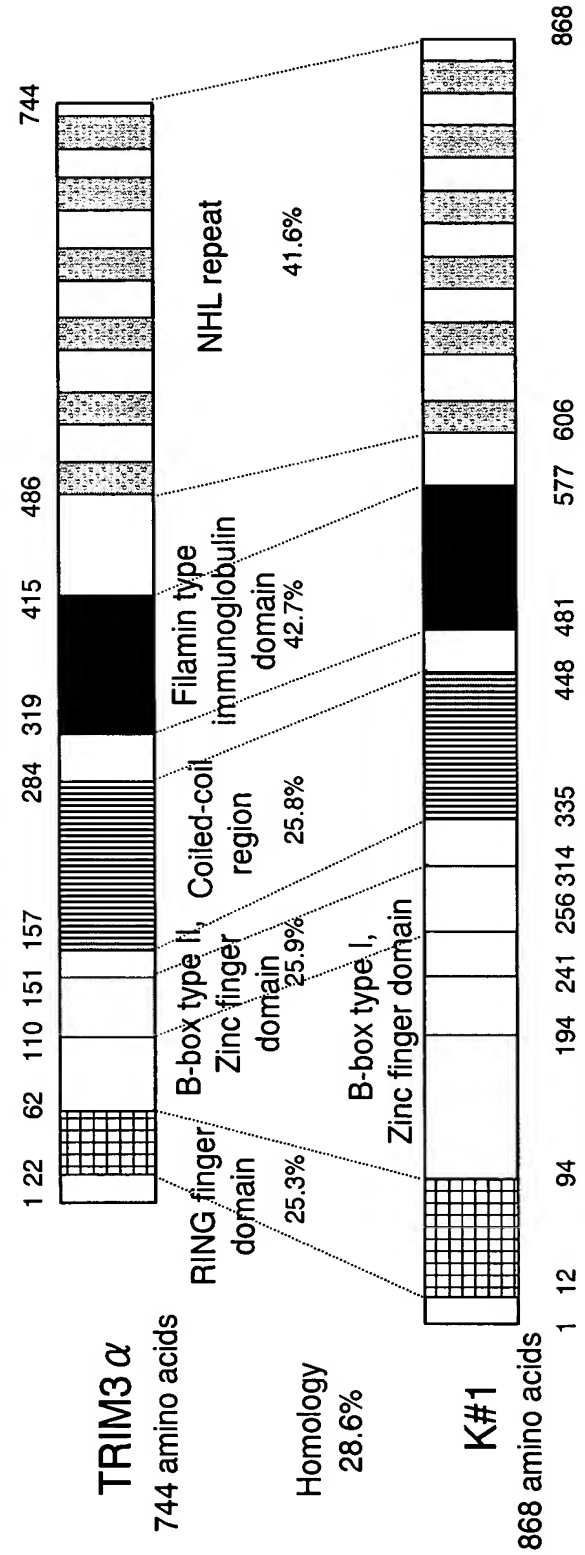
TRIM3 α
744 amino acids
1 22 62 110 151 157 284 319 415 486 744
RING finger domain
B-box type II, Zinc finger domain
Coiled-coil region
Filamin type immunoglobulin domain
NHL repeat
25.3%
25.9%
25.8%
42.7%
41.6%
Homology 28.6%
K#1
868 amino acids
1 12 94 194 241 256 314 335 448 481 577 606 868
B-box type I, Zinc finger domain

FIG. 69

```
GTAATTGACAAAGTCACGTGTGCTCAGGGGGCCAGAAACTGGAGAGAGGAGAGAAAAAAA   60
TCAAAAGAAGGAAAGCACATTAGACCATGCGAGCTAAATTTGTGATCGCACAAAATCAAG  120
ATGTTAGATTGATGCAGAAGATCACTCCGTTCCAAAGGGAAAGTTTTCATCTCACGAGTT  180
TGGAGCTGAGGGCCCGTGGGGCAACATGGCCGAAGGCGGGGCTAGCAAAGGTGGTGGAGA  240
                                MetAlaGluGlyGlyAlaSerLysGlyGlyGlyGlu   12

AGAGCCCGGGAAGCTGCCGGAGCCGGCAGAGGAGGAATCCCAGGTTTTGCGCGGAACTGG  300
 GluProGlyLysLeuProGluProAlaGluGluGluSerGlnValLeuArgGlyThrGly   32

CCACTGTAAGTGGTTCAATGTGCGCATGGGATTTGGATTCATCTCCATGATAAACCGAGA  360
 HisCysLysTrpPheAsnValArgMetGlyPheGlyPheIleSerMetIleAsnArgGlu   52

GGGAAGCCCCTTGGATATTCCAGTCGATGTATTTGTACACCAAAGCAAACTATTCATGGA  420
 GlySerProLeuAspIleProValAspValPheValHisGlnSerLysLeuPheMetGlu   72

AGGATTTAGAAGCCTAAAAGAAGGAGAACCAGTGGAATTCACATTTAAAAAATCTTCCAA  480
 GlyPheArgSerLeuLysGluGlyGluProValGluPheThrPheLysLysSerSerLys   92

AGGCCTTGAGTCAATACGGGTAACAGGACCTGGTGGGAGCCCCTGTTTAGGAAGTGAAAG  540
 GlyLeuGluSerIleArgValThrGlyProGlyGlySerProCysLeuGlySerGluArg  112

AAGACCCAAAGGGAAGACACTACAGAAAAGAAAACCAAAGGGAGATAGATGCTACAACTG  600
 ArgProLysGlyLysThrLeuGlnLysArgLysProLysGlyAspArgCysTyrAsnCys  132

TGGTGGCCTTGATCATCATGCTAAGGAATGTAGTCTACCTCCTCAGCCAAAGAAGTGCCA  660
 GlyGlyLeuAspHisHisAlaLysGluCysSerLeuProProGlnProLysLysCysHis  152

TTACTGTCAGAGCATCATGCACATGGTGGCAAACTGCCCACATAAAAATGTTGCACAGCC  720
 TyrCysGlnSerIleMetHisMetValAlaAsnCysProHisLysAsnValAlaGlnPro  172

ACCCGCGAGTTCTCAGGGAAGACAGGAAGCAGAATCCCAGCCATGCACTTCAACTCTCCC  780
 ProAlaSerSerGlnGlyArgGlnGluAlaGluSerGlnProCysThrSerThrLeuPro  192

TCGAGAAGTGGGAGGCGGGCATGGCTGTACATCACCACCGTTTCCTCAGGAGGCTAGGGC  840
 ArgGluValGlyGlyGlyHisGlyCysThrSerProProProGlnGluAlaArgAla  212

AGAGATCTCAGAACGGTCAGGCAGGTCACCTCAAGAAGCTTCCTCCACGAAGTCATCTAT  900
 GluIleSerGluArgSerGlyArgSerProGlnGluAlaSerSerThrLysSerSerIle  232

AGCACCAGAAGAGCAAAGCAAAAAGGGGCCTTCAGTTCAAAAAAGGAAAAAGACATAACA  960
 AlaProGluGluGlnSerLysLysGlyProSerValGlnLysArgLysLysThr***      250
```

FIG. 70

GGTCTTCTTCATATGTTCTTTCCTTTACCCGGTTGCAAAGTCTACCTCATGCAAGTATAG 1020
GGGAACAGTATTTCACAAGCAGTAGCTGACCTGGGATTTTAACTACTATTGGGGAACTGT 1080
GAATTTTTTAAACAGACAAATCACTCTAAGCAAATTACATTTGAGCAGGGTGTCATGTTT 1140
TATGTTAATTCAGAGAATAAGATACTATGTCTGTCAATATGTGCATGTGTGAGAGGGAGA 1200
GAGCCTGAGTCTGTGTGTGTACATGAGGATTTTTATATAGGAATGTAGACACATATATAA 1260
AGAGGCTTTGTCTTTATATATTTGTGTATAGATCAAAGCACACACCCTCTCTCATATAAT 1320
TGGATATTTCCAAGAATTGAAAACCCATGTGAAGCATTATAGATAGTTTTAAATTTAACC 1380
CACTGGAGTTTTCTTGAAATACCACTTCTTTTATATTATATAAAACTAAAAACACGACTG 1440
TTACCTTTTGTGTGAACCAAAGGATACTTCAGATCTCAGAGCTGCCAATTATGGGGTACT 1500
AAAGGTTTTTAAGACATCCAGTTCTCCCGAATTTGGGATTGCCTCTTTTTCTTGAAATCT 1560
CTGGAGTAGTAATTTTTTTCCCCCTTTTTTGAAGGCAGTACCTTAACTTCATATGCCTCT 1620
GACTGCCATAAGCTTTTTTGATTCTGGGATAACATAACTCCAGAAAAGACAATGAATGTG 1680
TAATTTGGGCCGATATTTCACTGTTTTAAATTCTGTGTTTAATTGTAAAATTAGATGCCT 1740
ATTAAGAGAAATGAAGGGGAGGATCATCTTAGTGGCTTGTTTTCAGTAGTATTTTAATAT 1800
CAGCTTCTTGTAACCTTTTCCATGTTGTGAGGGTTGTAAGGGATTGTGTGGCAACAGCAG 1860
CTTCCCTTGGCTAACTCAATCTTCTACCCATTGCTTAGAGCAGGGAGCCCTCCTTATTTA 1920
CTACTGAAGACCTTAGAGAACTCCAATTGTTTGGCATATATTTTTGGTGGTGGTTTTTAT 1980
TCCTCCTGGAGAGTTATCTAATTTGTTTCTAAAACAAACAAGCAGCAAAGAAATGAATTA 2040
AATACTGGGGTTGAGAATTAAAATTAAGTGGATGTTCACAGTTGCCCAATATATATGACC 2100
TGCAAATGATACGAAAAAGTGCAGCATTTAGTGGCAGTTAACAAGAGTGACAAGCCTGGG 2160
GCAGAGGTACCAAACCTCTCCCACCAGAGAGCTAGAAGTATTTTATACAGTAACTTTGAT 2220
CTTATGGAAGTGACCTTCAATGCTTATTCTGAAGTAACCTATATGGTGGATACAGGATGA 2280
ACATTCAGTGCCAGGGAGAATCTTCTCAGGTTGGTTCTCGTTAGAGTGATAAACTGGCTA 2340
GGGGCCATAGTATTGGTCCTGTTAGGTTTCGGTCATGGAAAAAAAAATTATTTTGGGGTC 2400
ATCCTGGCTCTAGATGTTATGGGCAAATTTCTGAAACATCTGCAAGAAGGTACCAGTTAA 2460
TTATAGTGCTTAATATTGGGAATAAGATTAAGCATTATAATTATAATGTATGGGCCTGTT 2520
GGTGTAAGCTCAGATAATTAAATAAAAATAGCATGACTCAAATGAGACATATTCTGCTGA 2580
ACAGTTTCTACTTCCTCTCCCGCCTGTCCTGTCATGGGAGACGTGTATAGTTGCTGCTGT 2640
TTCAGCAAACCACCATAAGACGAAAATGCCTCAGGTTGGGTTGCCAGTCCTTTACAACTC 2700
AGCTTGAATTTCACAACAGTGATTGTGAGAATCTGCGTGGTATACACTGAAATATCGGTG 2760
TGCTGTGATGCAAAGCTTACCTTTGACGATATTGAATGTGATATAGCTGTAGAGAAGTAC 2820
TTCCTTGCCTTATGTGAGGATTTCAAACTTATTTAAATTATGTAGACAAATCAAAGTGGC 2880
ATTGCTTAATTTTTAGCAGGCATAATAAGCAAGTTAACAGTAAAATGCAAAACATGATAA 2940
GCGTTGCTCAATTTTTAGCAGGTATAATAAGCAGGTTAACAGTAAAAATGCAAAACATGA 3000
TAGATAAGTCACTTTGAAAATTCAAACCAAAGTTCCTTCACCTTATGGAAATAGGAAATT 3060
ATGGACTTCAAAATTGGACACTTCCTGTTTACAAAAAGAAATTCAGAGCTAAAATCATGG 3120
TAAAAAAAAATAGAAACACTTGAGAACTATGGTCTTTATGGGTGCAATTTGAAATCCTTT 3180
TCATCATCTTACCAGACTAAACTAAGAGCACATACCAAACCTATCTTATGGTTGAAAGTT 3240
GGGGTTTATTTTTTATATGAGAATATTATCACTATTACATAACATACTCAGGACAAAGAA 3300
CTTTGCTCAGGGAACATACCATGTAATATTTTTGTTGTTTCTTTACAGACTAGTCTACAG 3360
TCCTGCTTACTCAAAACAAACCAAATAACTTATACCTTTATATAAGTATTATGTACTGAT 3420

FIG. 70 (continued from previous page)

GATAGTAACTACCTCTGAGTTTGACACAGATCAAAATTTTTGAATATCAGATATCAGTTA 3480
TCCTATTTTTATTTCATGTGAAAACTCCTCTAAAGCAGATTCCCTCAACTCTGTGCATAT 3540
GTGAATATCACTGATGTGAACACATTGTTCATTTACATAGGTAAAATATTACTCTGTTTA 3600
CAGCAAAAGGCTACCTCATAGTTGATACATAGCACACCTGTATGTATGCTGTTCCAGCCT 3660
TACAGGTGGCTGATAATTCTCTGGTACAGAACCTTTTTATCTGTATTATAAATAGCAATT 3720
CACAACTGCATGTTTCTGACAAACACTTGTGAATAATGAAGCATCTCGTTTTAGTTAGCA 3780
AAGTCTCCAAACATTTCCTTAAAATAATCATGTATTTAGTTTAAAGAATTATGGGCACTG 3840
TTCAACTTAAGCAAAACAGAACACGGAAGCAGTCTTAGAAGCACCACTTTGCCCAGAGGT 3900
GGAGGTTGGAAGGGGTAGCAGGGAGAGGGGTTGGTGTATGCAGGTATTCATGCTAGGCAA 3960
AGAGTTTAAAAGACGCCAATGTCCTTCATTTACTGTCTGTGCTGCCCTGAAGCCAAGCGT 4020
ATTGCAGCATTATAGCCCCAGGCACATAACTAACTAGCACTGGCTTGCCAAGGAATGAAC 4080
ATGCAATGCCATTACTAGCTATTGAGGGAAAAGGGTCTGTGTGAAGCATCACTTTGCAGG 4140
GATTACTAATGGTGGGGCAGCAGGTCTGTGAATTAAGTTATCTCTTGACCTCACCCTCAT 4200
GTCAACACAAATGTAATTCCTAAACAAGATGCATTGCCAGTCTCTTAGCCCTGTAAGCTG 4260
ATCTTTTGCTACATGGCAGACTATAATGAAAACATTTTTATACTTGGGTTTCTAGTCTTC 4320
ACTAGAAGGCCTTGGATGTATTTTTGCAGTTGAAAGATTTAGAAAGATTTTTACCTGCTT 4380
ATAACTTGGAAGTTTAGAGTGCAATGTAAGAAAAAAGATCAAGAAATGTCATGTTATTAG 4440
CATCAGTCCACCTCCAATATTGCCGATACTTTTTTTATTCTGGCTCAGTTTTATTTTGCA 4500
CCAGTGCGGCCCCAAGTTACTGCTGGTTGTATTTAGTTTGTGAATAGGAGCCCATAAGTG 4560
TTAATAGACTTTGTAACATTCACTATAAGATGAATTATACAGGACATGGGAAATCTCATT 4620
AAGTCTTAAAGTTAATTTAAATTAATTTATCTGTTTTCTCTAAGAAATGTTTATCATAAA 4680
ATATATATGTGTATTTCCCCTTTGGTTATAAAATTTGGGAAAGTATGTACAAGTGCAGCT 4740
GCACTGACTTTAATTTTCTAGATGTCTTAATGAGATTTATTTGTTTTAGAGAAGAACATC 4800
TTGTTAAAAGCATCAAACTCTGTCTTACATAGCTGTCAACAGCCTCTTTAAGATGTGGTG 4860
GTTGTATGATCTGTGTCTTAATTGTTCAGTTAGAGTGAGAAGTTGACCTATGATTCATTT 4920
TTAAATTTTATATTTGGAACAAAGCTGCAAGTTATGGTAAAGTACTGTACTGTGAGAAGT 4980
ATTATGATATTTAATGCATCTGTGGCTTAACACTTGTGAGAGTTACCAGCTTGAAAATGA 5040
TGGTGTTGACTACCTCTTGAATCACATCTATCAACCACTGGCACCTACCACCAAGCTGGC 5100
TTCAATTAGTATGTGTTGCTTTTTGGTATTAACAACTAACCGTACTAGAGACCAAAGTGA 5160
ACCCTGATTTTTATATGTCTTTAATAATGGTGTTTTATCTAGTGTTTTTAAATTATCCTG 5220
TGTAGTATTTAGATTACCTCATTGTCCATTTTGACTCATGTTGTTTACAAGTGAAAATAA 5280
AAACACTTGAACTGTATGTTTTTAAAAGACAAAAAAGGGGTAGATGTTTGGAATGCGTTT 5340
CACTCGCATGCAGTCATCTGGAGGGACTGAAGCACTGTTTGCCTTTCTGTACACTCTGGG 5400
TTTTATATTCTCATTTCATGCCTAATGTCTTATTCTGTCAATTATGGATATGTTGAGGTT 5460
TAAAAAAATTACTTGATTAAAAATAAAACATATAACGTTGGCATTTAAAAAAAAAAAAAA 5520
AAAAAAAAAAAAAAAAAAAAA 5542

FIG. 70 (continued from previous page)

```
AGTAGCTCTAAACCATCTTCACGATTTCTCTTTCCTCCTCGTGCCCGCCGGAGAGAATAG      60
TTTCGCTGAAAATTTCTCTTTGTCAATGGGATCAGTATTAAATCAGCAATATACAAGTAA     120
AGTATCGCATGCTGTAATGTAAAATGTGGCTGAAAAATGGAGTTAAATGAATAAGTACAC     180
GCGGGGCTAGCAAAGGTGGTGGAGAAGAGCCCGGGAAGCTGCCGGAGCCGGCAGAGGAGG     240
AATCCCAGGTTTTGCGCGGAACTGGCCACTGTAAGTGGTTCAATGTGCGCATGGGATTTG     300
                                                  MetGlyPheGly       4

GATTCATCTCCATGATAAACCGAGAGGGAAGCCCCTTGGATATTCCAGTCGATGTATTTG     360
  PheIleSerMETIleAsnArgGluGlySerProLeuAspIleProValAspValPheVal      24

TACACCAAAGCAAACTATTCATGGAAGGATTTAGAAGCCTAAAAGAAGGAGAACCAGTGG     420
  HisGlnSerLysLeuPheMETGluGlyPheArgSerLeuLysGluGlyGluProValGlu      44

AATTCACATTTAAAAAATCTTCCAAAGGCCTTGAGTCAATACGGGTAACAGGACCTGGTG     480
  PheThrPheLysLysSerSerLysGlyLeuGluSerIleArgValThrGlyProGlyGly      64

GGAGCCCCTGTTTAGGAAGTGAAAGAAGACCCAAAGGGAAGACACTACAGAAAAGAAAAC     540
  SerProCysLeuGlySerGluArgArgProLysGlyLysThrLeuGlnLysArgLysPro      84

CAAAGGGAGATAGATGCTACAACTGTGGTGGCCTTGATCATCATGCTAAGGAATGTAGTC     600
  LysGlyAspArgCysTyrAsnCysGlyGlyLeuAspHisHisAlaLysGluCysSerLeu     104

TACCTCCTCAGCCAAAGAAGTGCCATTACTGTCAGAGCATCATGCACATGGTGGCAAACT     660
  ProProGlnProLysLysCysHisTyrCysGlnSerIleMETHisMETValAlaAsnCys     124

GCCCACATAAAAATGTTGCACAGCCACCCGCGAGTTCTCAGGGAAGACAGGAAGCAGAAT     720
  ProHisLysAsnValAlaGlnProProAlaSerSerGlnGlyArgGlnGluAlaGluSer     144

CCCAGCCATGCACTTCAACTCTCCCTCGAGAAGTGGGAGGCGGGCATGGCTGTACATCAC     780
  GlnProCysThrSerThrLeuProArgGluValGlyGlyGlyHisGlyCysThrSerPro     164

CACCGTTTCCTCAGGAGGCTAGGGCAGAGATCTCAGAACGGTCAGGCAGGTCACCTCAAG     840
  ProPheProGlnGluAlaArgAlaGluIleSerGluArgSerGlyArgSerProGlnGlu     184

AAGCTTCCTCCACGAAGTCATCTATAGCACCAGAAGAGCAAAGCAAAAAGGGGCCTTCAG     900
  AlaSerSerThrLysSerSerIleAlaProGluGluGlnSerLysLysGlyProSerVal     204

TTCAAAAAAGGAAAAAGACATAACAGGTCTTCTTCATATGTTCTTTCCTTTACCCGGTTG     960
  GlnLysArgLysLysThr***                                            210
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FIG. 71

CAAAGTCTACCTCATGCAAGTATAGGGGAACAGTATTTCACAAGCAGTAGCTGACCTGGG 1020
ATTTTAACTACTATTGGGGAACTGTGAATTTTTTAAACAGACAAATCACTCTAAGCAAAT 1080
TACATTTGAGCAGGGTGTCATGTTTTATGTTAATTCAGAGAATAAGATACTATGTCTGTC 1140
AATATGTGCATGTGTGAGAGGGAGAGAGCCTGAGTCTGTGTGTGTACATGAGGATTTTTA 1200
TATAGGAATGTAGACACATATATAAAGAGGCTTTGTCTTTATATATTTGTGTATAGATCA 1260
AAGCACACACCCTCTCTCATATAATTGGATATTTCCAAGAATTGAAAACCCATGTGAAGC 1320
ATTATAGATAGTTTTAAATTTAACCCACTGGAGTTTTCTTGAAATACCACTTCTTTTATA 1380
TTATATAAAACTAAAAACACGACTGTTACCTTTTGTGTGAACCAAAGGATACTTCAGATC 1440
TCAGAGCTGCCAATTATGGGGTACTAAAGGTTTTTAAGACATCCAGTTCTCCCGAATTTG 1500
GGATTGCCTCTTTTTCTTGAAATCTCTGGAGTAGTAATTTTTTTCCCCCTTTTTTGAAGG 1560
CAGTACCTTAACTTCATATGCCTCTGACTGCCATAAGCTTTTTTGATTCTGGGATAACAT 1620
AACTCCAGAAAAGACAATGAATGTGTAATTTGGGCCGATATTTCACTGTTTTAAATTCTG 1680
TGTTTAATTGTAAAATTAGATGCCTATTAAGAGAAATGAAGGGGAGGATCATCTTAGTGG 1740
CTTGTTTTCAGTAGTATTTTAATATCAGCTTCTTGTAACCTTTTCCATGTTGTGAGGGTT 1800
GTAAGGGATTGTGTGGCAACAGCAGCTTCCCTTGGCTAACTCAATCTTCTACCCATTGCT 1860
TAGAGCAGGGAGCCCTCCTTATTTACTACTGAAGACCTTAGAGAACTCCAATTGTTTGGC 1920
ATATATTTTTGGTGGTGGTTTTTATTCCTCCTGGAGAGTTATCTAATTTGTTTCTAAAAC 1980
AAACAAGCAGCAAAGAAATGAATTAAATACTGGGGTTGAGAATTAAAATTAAGTGGATGT 2040
TCACAGTTGCCCAATATATATGACCTGCAAATGATACGAAAAAGTGCAGCATTTAGTGGC 2100
AGTTAACAAGAGTGACAAGCCTGGGGCAGAGGTACCAAACCTCTCCCACCAGAGAGCTAG 2160
AAGTATTTTATACAGTAACTTTGATCTTATGGAAGTGACCTTCAATGCTTATTCTGAAGT 2220
AACCTATATGGTGGATACAGGATGAACATTCAGTGCCAGGGAGAATCTTCTCAGGTTGGT 2280
TCTCGTTAGAGTGATAAACTGGCTAGGGGCCATAGTATTGGTCCTGTTAGGTTTCGGTCA 2340
TGGAAAAAAAAATTATTTTGGGGTCATCCTGGCTCTAGATGTTATGGGCAAATTTCTGAA 2400
ACATCTGCAAGAAGGTACCAGTTAATTATAGTGCTTAATATTGGGAATAAGATTAAGCAT 2460
TATAATTATAATGTATGGGCCTGTTGGTGTAAGCTCAGATAATTAAATAAAAATAGCATG 2520
ACTCAAATGAGACATATTCTGCTGAACAGTTTCTACTTCCTCTCCCGCCTGTCCTGTCAT 2580
GGGAGACGTGTATAGTTGCTGCTGTTTCAGCAAACCACCATAAGACGAAAATGCCTCAGG 2640
TTGGGTTGCCAGTCCTTTACAACTCAGCTTGAATTTCACAACAGTGATTGTGAGAATCTG 2700
CGTGGTATACACTGAAATATCGGTGTGCTGTGATGCAAAGCTTACCTTTGACGATATTGA 2760
ATGTGATATAGCTGTAGAGAAGTACTTCCTTGCCTTATGTGAGGATTTCAAACTTATTTA 2820
AATTATGTAGACAAATCAAAGTGGCATTGCTTAATTTTTAGCAGGCATAATAAGCAAGTT 2880
AACAGTAAAATGCAAAACATGATAAGCGTTGCTCAATTTTTAGCAGGTATAATAAGCAGG 2940
TTAACAGTAAAAATGCAAAACATGATAGATAAGTCACTTTGAAAATTCAAACCAAAGTTC 3000
CTTCACCTTATGGAAATAGGAAATTATGGACTTCAAAATTGGACACTTCCTGTTTACAAA 3060
AAGAAATTCAGAGCTAAAATCATGGTAAAAAAAAATAGAAACACTTGAGAACTATGGTCT 3120
TTATGGGTGCAATTTGAAATCCTTTTCATCATCTTACCAGACTAAACTAAGAGCACATAC 3180
CAAACCTATCTTATGGTTGAAAGTTGGGGTTTATTTTTTATATGAGAATATTATCACTAT 3240
TACATAACATACTCAGGACAAAGAACTTTGCTCAGGGAACATACCATGTAATATTTTTGT 3300
TGTTTCTTTACAGACTAGTCTACAGTCCTGCTTACTCAAAACAAACCAAATAACTTATAC 3360
CTTTATATAAGTATTATGTACTGATGATAGTAACTACCTCTGAGTTTGACACAGATCAAA 3420
ATTTTTGAATATCAGATATCAGTTATCCTATTTTTATTTCATGTGAAAACTCCTCTAAAG 3480

FIG. 71 (continued from previous page)

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CAGATTCCCTCAACTCTGTGCATATGTGAATATCACTGATGTGAACACATTGTTCATTTA 3540
CATAGGTAAAATATTACTCTGTTTACAGCAAAAGGCTACCTCATAGTTGATACATAGCAC 3600
ACCTGTATGTATGCTGTTCCAGCCTTACAGGTGGCTGATAATTCTCTGGTACAGAACCTT 3660
TTTATCTGTATTATAAATAGCAATTCACAACTGCATGTTTCTGACAAACACTTGTGAATA 3720
ATGAAGCATCTCGTTTTAGTTAGCAAAGTCTCCAAACATTTCCTTAAAATAATCATGTAT 3780
TTAGTTTAAAGAATTATGGGCACTGTTCAACTTAAGCAAAACAGAACACGGAAGCAGTCT 3840
TAGAAGCACCACTTTGCCCAGAGGTGGAGGTTGGAAGGGGTAGCAGGGAGAGGGGTTGGT 3900
GTATGCAGGTATTCATGCTAGGCAAAGAGTTTAAAAGACGCCAATGTCCTTCATTTACTG 3960
TCTGTGCTGCCCTGAAGCCAAGCGTATTGCAGCATTATAGCCCCAGGCACATAACTAACT 4020
AGCACTGGCTTGCCAAGGAATGAACATGCAATGCCATTACTAGCTATTGAGGGAAAAGGG 4080
TCTGTGTGAAGCATCACTTTGCAGGGATTACTAATGGTGGGGCAGCAGGTCTGTGAATTA 4140
AGTTATCTCTTGACCTCACCCTCATGTCAACACAAATGTAATTCCTAAACAAGATGCATT 4200
GCCAGTCTCTTAGCCCTGTAAGCTGATCTTTTGCTACATGGCAGACTATAATGAAAACAT 4260
TTTTATACTTGGGTTTCTAGTCTTCACTAGAAGGCCTTGGATGTATTTTTGCAGTTGAAA 4320
GATTTAGAAAGATTTTTACCTGCTTATAACTTGGAAGTTTAGAGTGCAATGTAAGAAAAA 4380
AGATCAAGAAATGTCATGTTATTAGCATCAGTCCACCTCCAATATTGCCGATACTTTTTT 4440
TATTCTGGCTCAGTTTTATTTTGCACCAGTGCGGCCCCAAGTTACTGCTGGTTGTATTTA 4500
GTTTGTGAATAGGAGCCCATAAGTGTTAATAGACTTTGTAACATTCACTATAAGATGAAT 4560
TATACAGGACATGGGAAATCTCATTAAGTCTTAAAGTTAATTTAAATTAATTTATCTGTT 4620
TTCTCTAAGAAATGTTTATCATAAAATATATATGTGTATTTCCCCTTTGGTTATAAAATT 4680
TGGGAAAGTATGTACAAGTGCAGCTGCACTGACTTTAATTTTCTAGATGTCTTAATGAGA 4740
TTTATTTGTTTTAGAGAAGAACATCTTGTTAAAAGCATCAAACTCTGTCTTACATAGCTG 4800
TCAACAGCCTCTTTAAGATGTGGTGGTTGTATGATCTGTGTCTTAATTGTTCAGTTAGAG 4860
TGAGAAGTTGACCTATGATTCATTTTTAAATTTTATATTTGGAACAAAGCTGCAAGTTAT 4920
GGTAAAGTACTGTACTGTGAGAAGTATTATGATATTTAATGCATCTGTGGCTTAACACTT 4980
GTGAGAGTTACCAGCTTGAAAATGATGGTGTTGACTACCTCTTGAATCACATCTATCAAC 5040
CACTGGCACCTACCACCAAGCTGGCTTCAATTAGTATGTGTTGCTTTTTGGTATTAACAA 5100
CTAACCGTACTAGAGACCAAAGTGAACCCTGATTTTTATATGTCTTTAATAATGGTGTTT 5160
TATCTAGTGTTTTTAAATTATCCTGTGTAGTATTTAGATTACCTCATTGTCCATTTTGAC 5220
TCATGTTGTTTACAAGTGAAAATAAAAACACTTGAACTGTATGTTTTTAAAAGACAAAAA 5280
AGGGGTAGATGTTTGGAATGCGTTTCACTCGCATGCAGTCATCTGGAGGGACTGAAGCAC 5340
TGTTTGCCTTTCTGTACACTCTGGGTTTTATATTCTCATTTCATGCCTAATGTCTTATTC 5400
TGTCAATTATGGATATGTTGAGGTTTAAAAAAATTACTTGATTAAAAATAAAACATATAA 5460
CGTTGGCATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5507
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FIG. 71 (continued from previous page)

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Human K#2      1:-----------------------MAEGGASKGGGEEPGKLPEPAEEESQVLRGTGHCKWFNVRMG  42
Human          1:-------------MGSVSNQQFAGGCAKAAEEAPEEAPEDAARAADEPQLLHGAGICKWFNVRMG  52
Mouse          1:-------------MGSVSNQQFAGGCAKAAEKAPEEAPPDAARAADEPQLLHGAGICKWFNVRMG  52
Xenopus        1:-------------------MGSVSNQEITEGLPKSLDGTADIHKSDKSVIFQGSGVCKWFNVRMG  46
Drosophila     1:--------------MENVQLENGLERRTTSQSSTSSANPANLASPTEECGCVRLGKCKWFNVAKG  51
C.elegans      1:MSTVVSEGRNDGNNRYSPQDEVEDRLPDVVDNRLTENMRVPSPERLPSPTPRYFGSCKWFNVSKG  65

Human K#2     43:FGFISMINREGSPLDIPVDVFVHQSKLFMEGFRSLKEGEPVEPTFKK--SSKGLESIRVTGP-GG 105
Human         53:FGFLSMTARAGVALDPPVDVFVHQSKLHMEGFRSLKEGEAVEFTFKK--SAKGLESIRVTGP-GG 115
Mouse         53:FGFLSMTARAGVALDPPVDVFVHQSKLHMEGFRSLKEGEAVEFTFKK--SAKGLESIRVTGP-GG 115
Xenopus       47:FGFLTMTKKEGTDLETPLDVFVHQSKLHMEGFRSLKEGESVEFTFKK--SSKGLESTQVTGP-GG 109
Drosophila    52:WGFLTPN--DGGQ-----EVFVHQSVIQMSGFRSLGEQEEVEFECQR--TSRGLEATRVSSR-HG 107
C.elegans     66:YGFVIDD-------ITGEDLFVHQSNLNMQGFRSLDEGERVSYYIQERSNGKGREAYAVSGEVEG 124
                                Cold shock domain(CSD)

Human K#2     106:SPCLGSERRPKGKTLQKRKPKGDRCYNCGGLD-HHAKECS-LPPQPKKCHYCQSIMHMVANCPHK 167
Human         116:VFCIGSERRPKGKSMQKRRSKGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQSISHMVASCPLK 177
Mouse         116:VFCIGSERRPKGKNMQKRRSKGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQSINHMVASCPLK 177
Xenopus       110:APCIGSERRPKVKGQQKRRQRGDRCYNCGGLD-HHAKECK-LPPQPKKCHFCQNPNHMVAQCPEK 171
Drosophila    108:GSCQGSTYRPRI---NRRTRRM-RCYNCGEFANHIASECA-LGPQPKRCHRCRGEDHLHADCPHK 166
C.elegans     125:QGLKGSRIHPLG---RKKAVSL-RCFRCGKFATHKAKSCPNVKTDAKVCYTCGSEEHVSSICPER 184
                                                Zinc finger domain

Human K#2     168:NVAQPPASSQGRQEAESQPCTSTLPREVGGGHGCTSPPFPQEARAEISERSGRSPQEASSTKSSI 232
Human         178:AQQGPSAQGKPTYFREEEEEIHSPTLLPEAQN                                209
Mouse         178:AQQGPSSQGKPAYF                                                  191
Xenopus       172:AMQAANLEDQPITEEQELIPEIME                                        195
Drosophila    167:NVTQSHSNSKSISNNSSSSAAQEKSEEAT                                   195
C.elegans     185:RRKHRPEQVAAEEAEAARMAAEKSSPTTSDDDIREKNSNSSDE                     227

Human K#2     233:APEEQSKKGPSVQKRKKT                                              250
```

FIG. 72

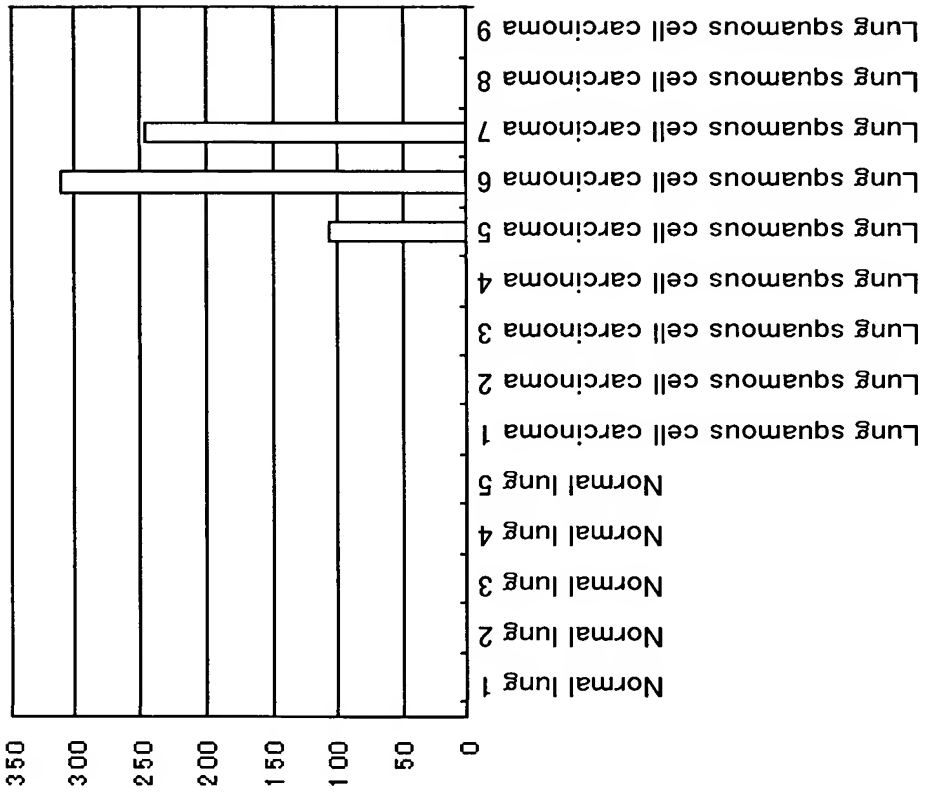

350
300
250
200
150
100
50
0
Normal lung 1
Normal lung 2
Normal lung 3
Normal lung 4
Normal lung 5
Lung squamous cell carcinoma 1
Lung squamous cell carcinoma 2
Lung squamous cell carcinoma 3
Lung squamous cell carcinoma 4
Lung squamous cell carcinoma 5
Lung squamous cell carcinoma 6
Lung squamous cell carcinoma 7
Lung squamous cell carcinoma 8
Lung squamous cell carcinoma 9

FIG. 73

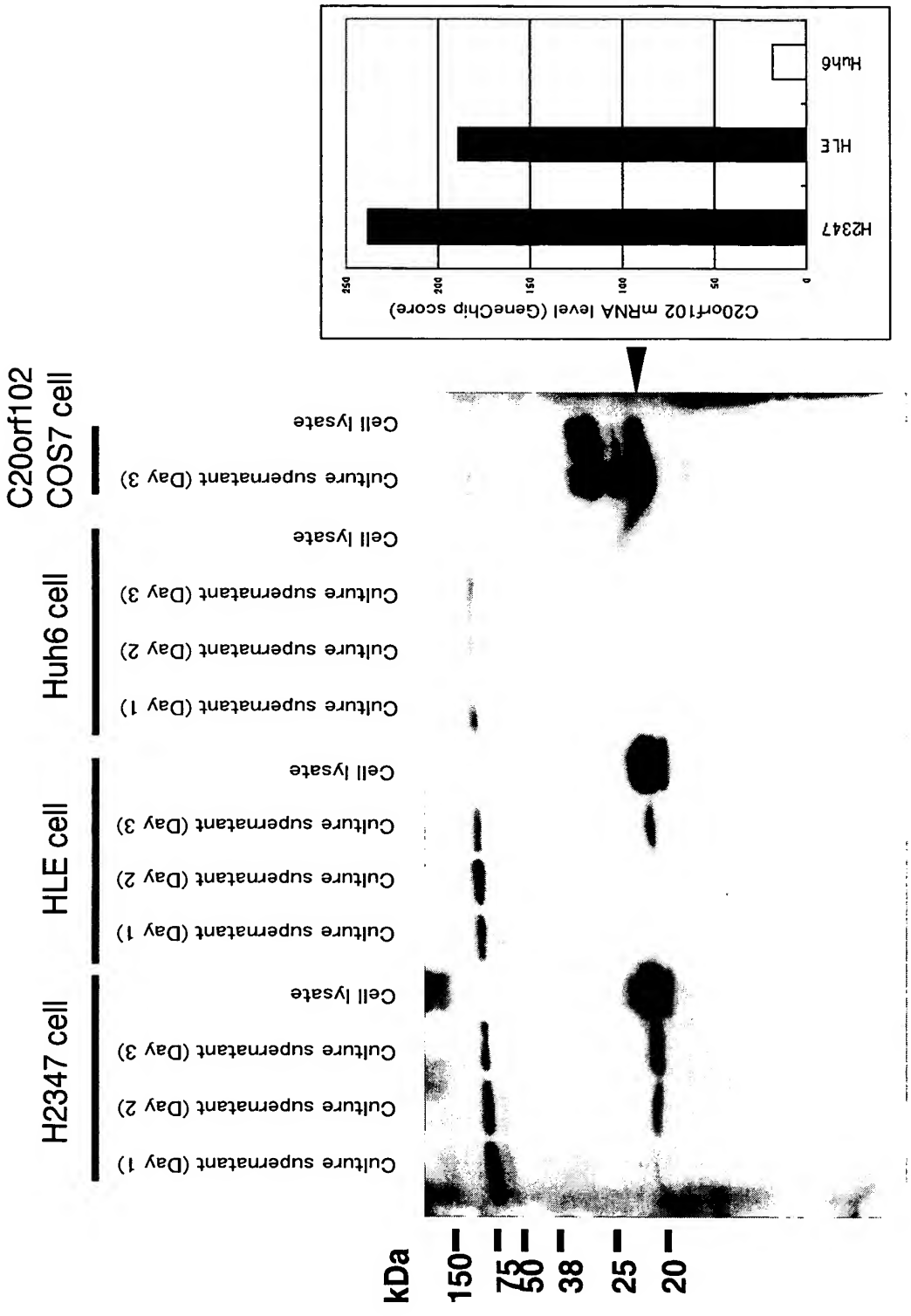

C20orf102 mRNA level (GeneChip score)
250
200
150
100
50
0
H2347
HLE
Huh6
C20orf102
COS7 cell
Huh6 cell
HLE cell
H2347 cell
Cell lysate
Culture supernatant (Day 3)
Culture supernatant (Day 2)
Culture supernatant (Day 1)
kDa
150
75
50
38
25
20

FIG. 74

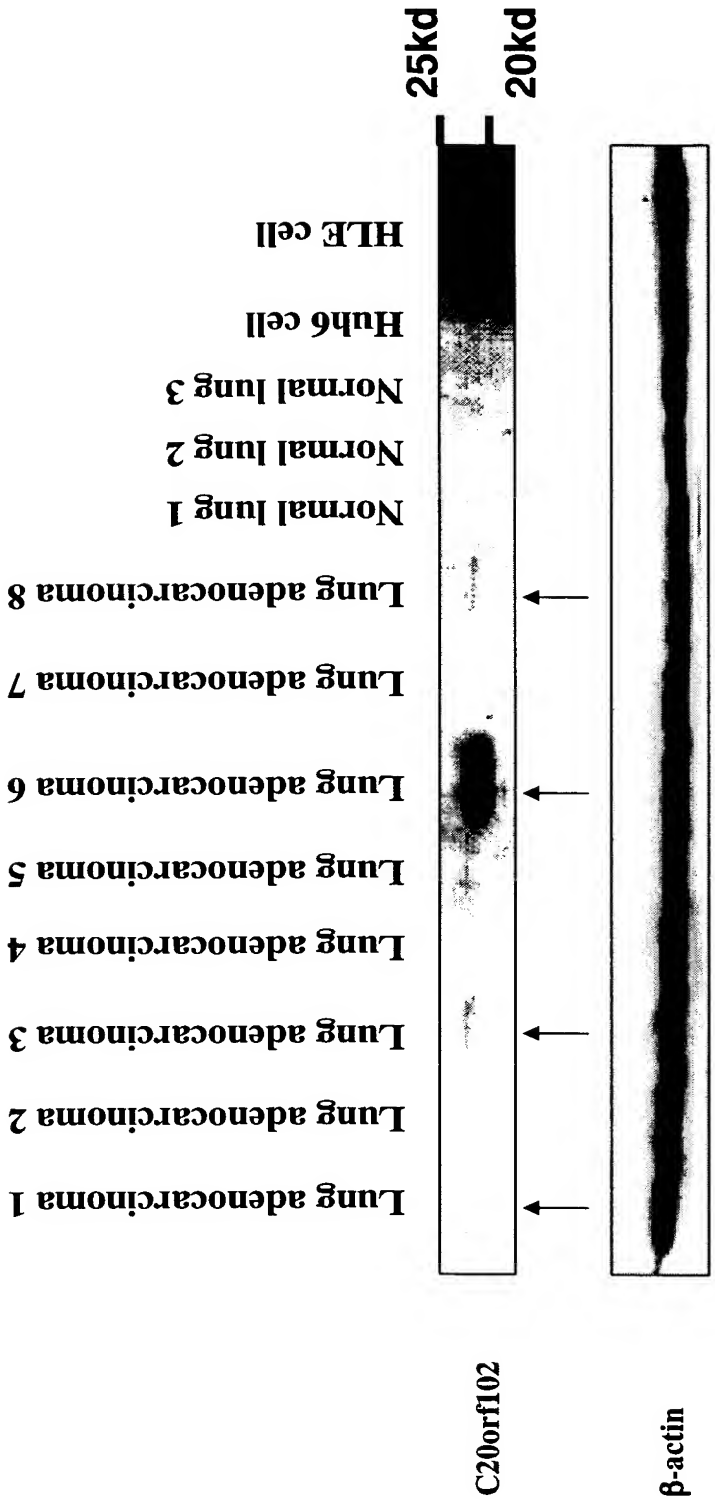
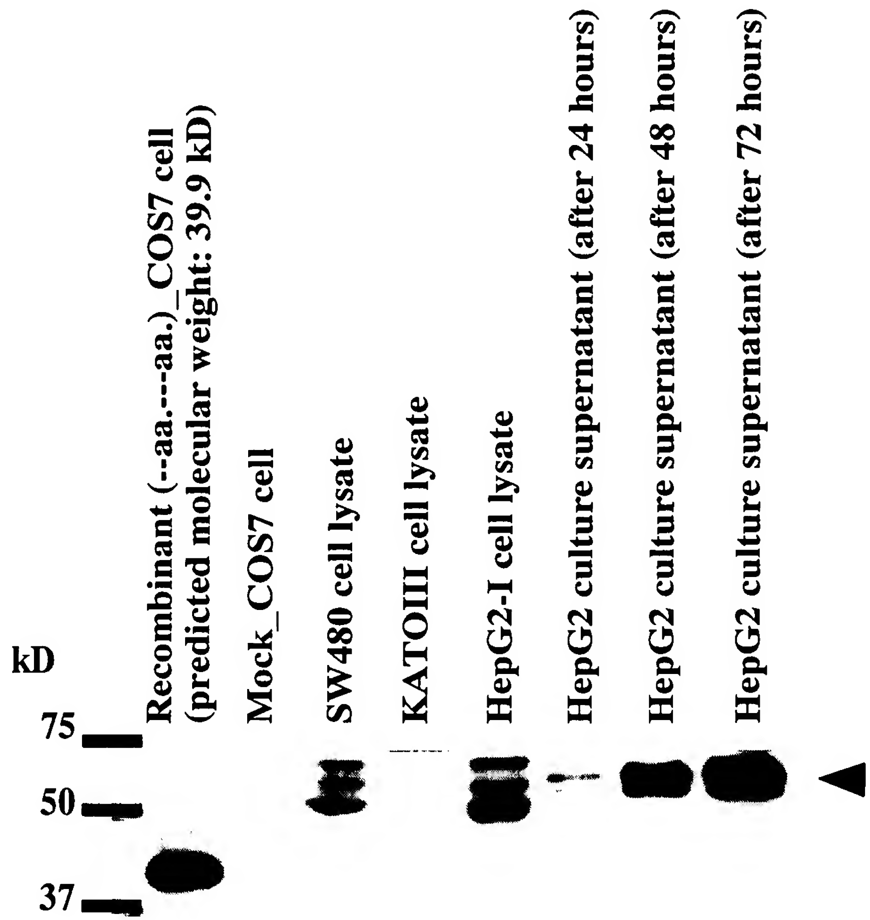
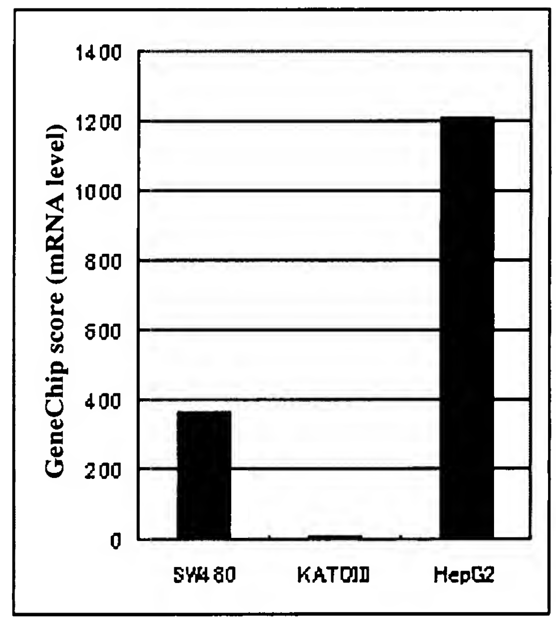

25kd
20kd
HLE cell
Huh6 cell
Normal lung 3
Normal lung 2
Normal lung 1
Lung adenocarcinoma 8
Lung adenocarcinoma 7
Lung adenocarcinoma 6
Lung adenocarcinoma 5
Lung adenocarcinoma 4
Lung adenocarcinoma 3
Lung adenocarcinoma 2
Lung adenocarcinoma 1
C20orf102
β-actin

FIG. 75





Predicted molecular weight: 55.7 kDa

FIG. 76

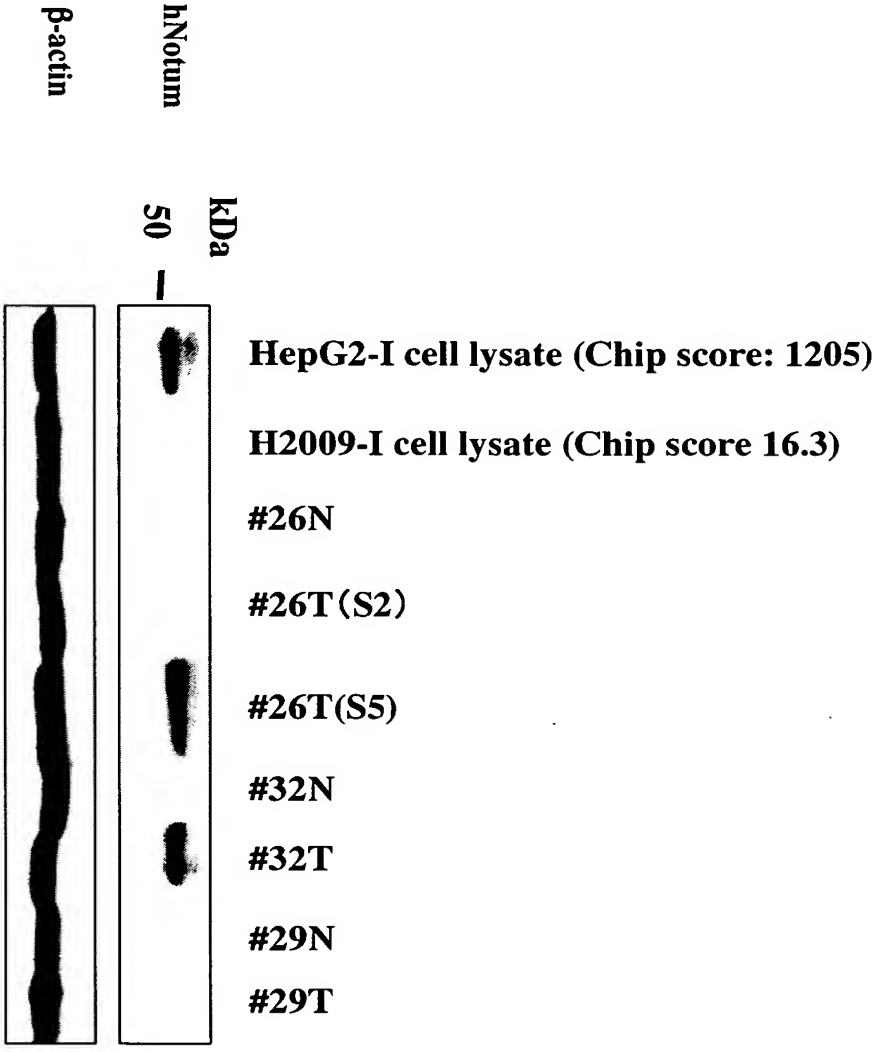
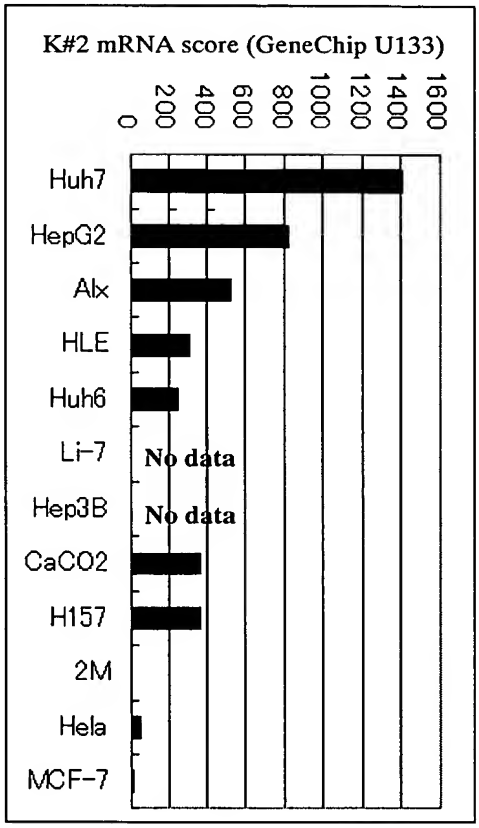

β-actin
hNotum
50
kDa
HepG2-I cell lysate (Chip score: 1205)
H2009-I cell lysate (Chip score 16.3)
#26N
#26T(S2)
#26T(S5)
#32N
#32T
#29N
#29T

FIG. 77

FIG. 78



1.K#2_HEK293
2.HuH7
3. HepG2
4.Alex
5. HLE
6.HuH6
7.Li-7
8.Hep3B
9.CaCO2
10.H157
11.2M
12.Hela
13.MCF-7

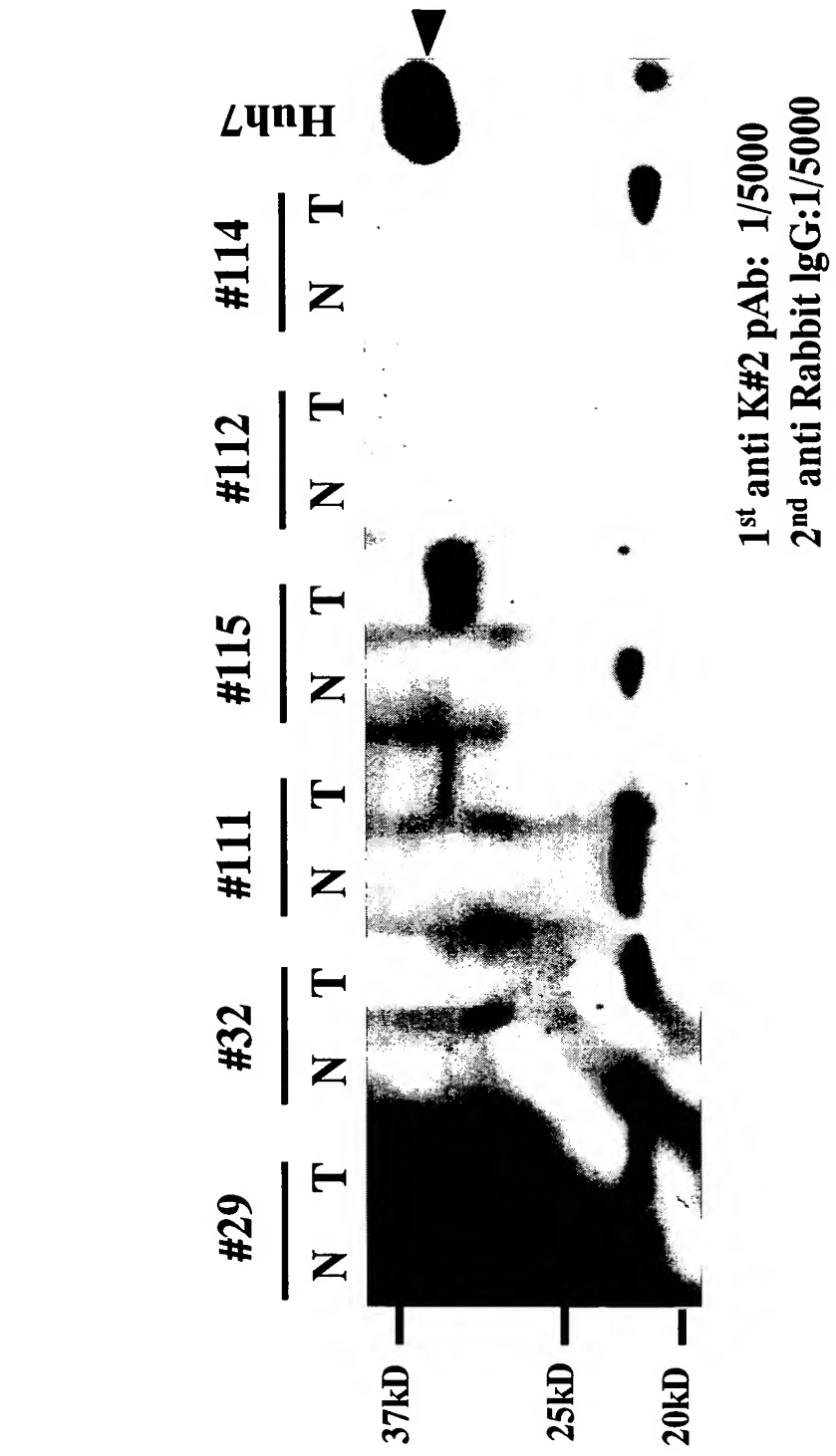
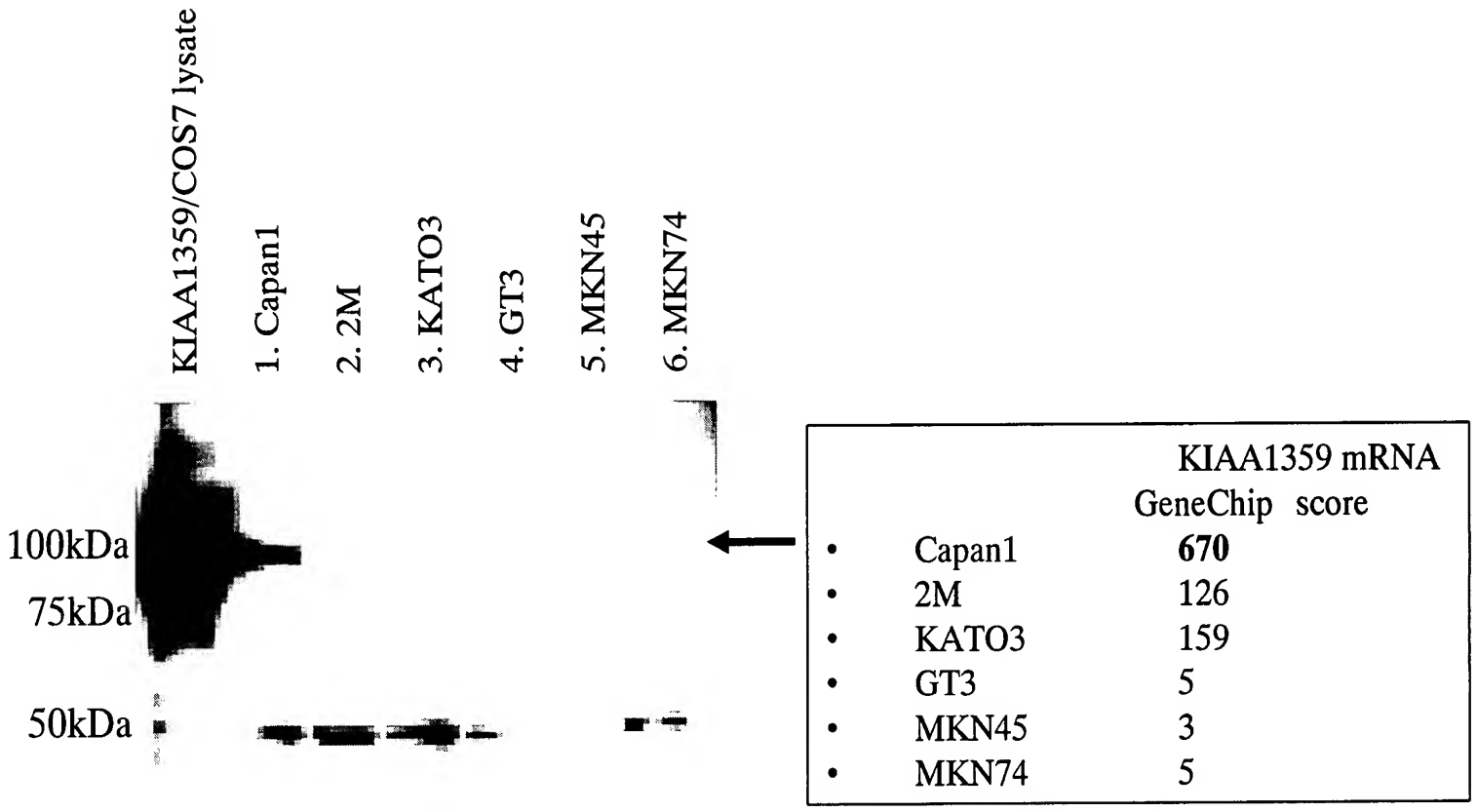

#29
N T
#32
N T
#111
N T
#115
N T
#112
N T
#114
N T
Huh7
37kD
25kD
20kD
1st anti K#2 pAb: 1/5000
2nd anti Rabbit lgG:1/5000

FIG. 79



Evaluation of A8409A

FIG. 80

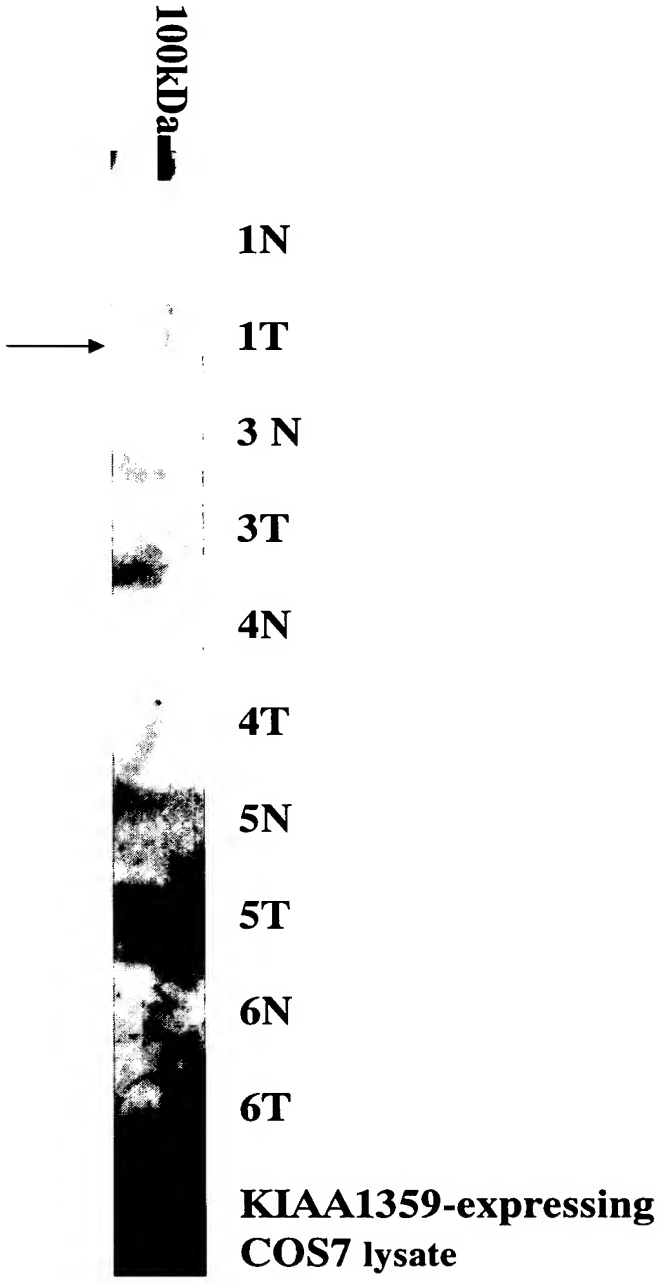

100kDa
1N
1T
3 N
3T
4N
4T
5N
5T
6N
6T
KIAA1359-expressing
COS7 lysate

FIG. 81

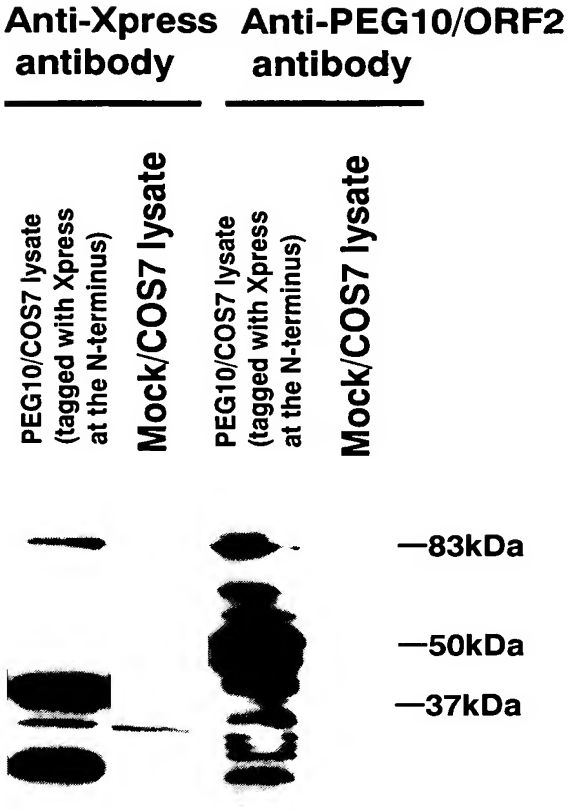

Anti-Xpress antibody
Anti-PEG10/ORF2 antibody
PEG10/COS7 lysate (tagged with Xpress at the N-terminus)
Mock/COS7 lysate
PEG10/COS7 lysate (tagged with Xpress at the N-terminus)
Mock/COS7 lysate
—83kDa
—50kDa
—37kDa

FIG. 82

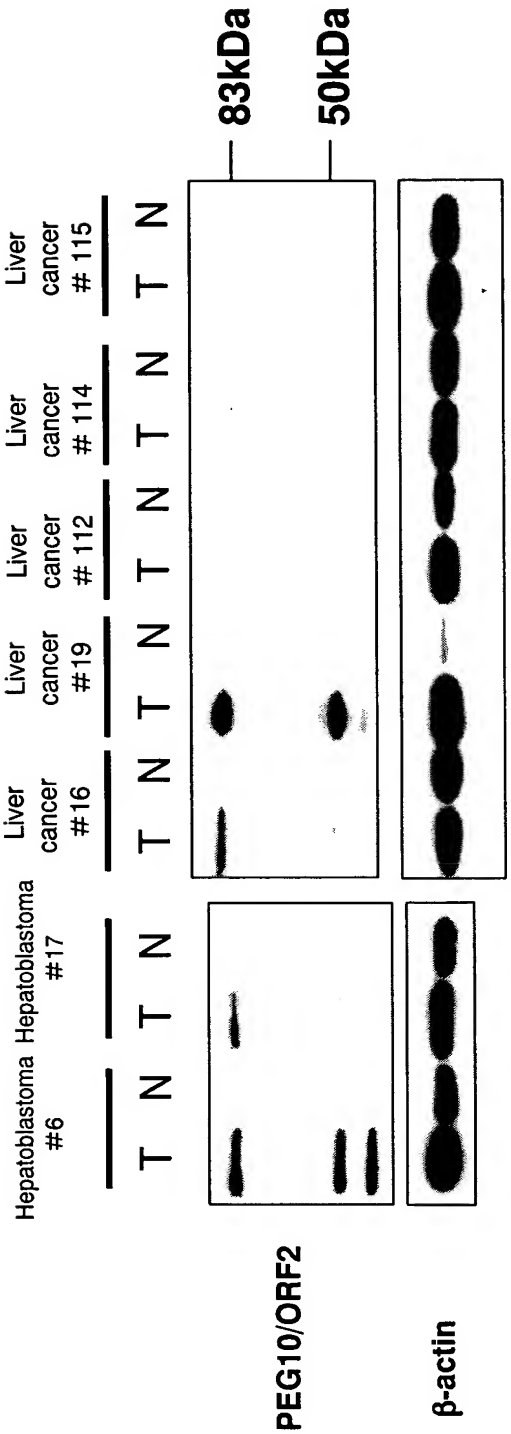
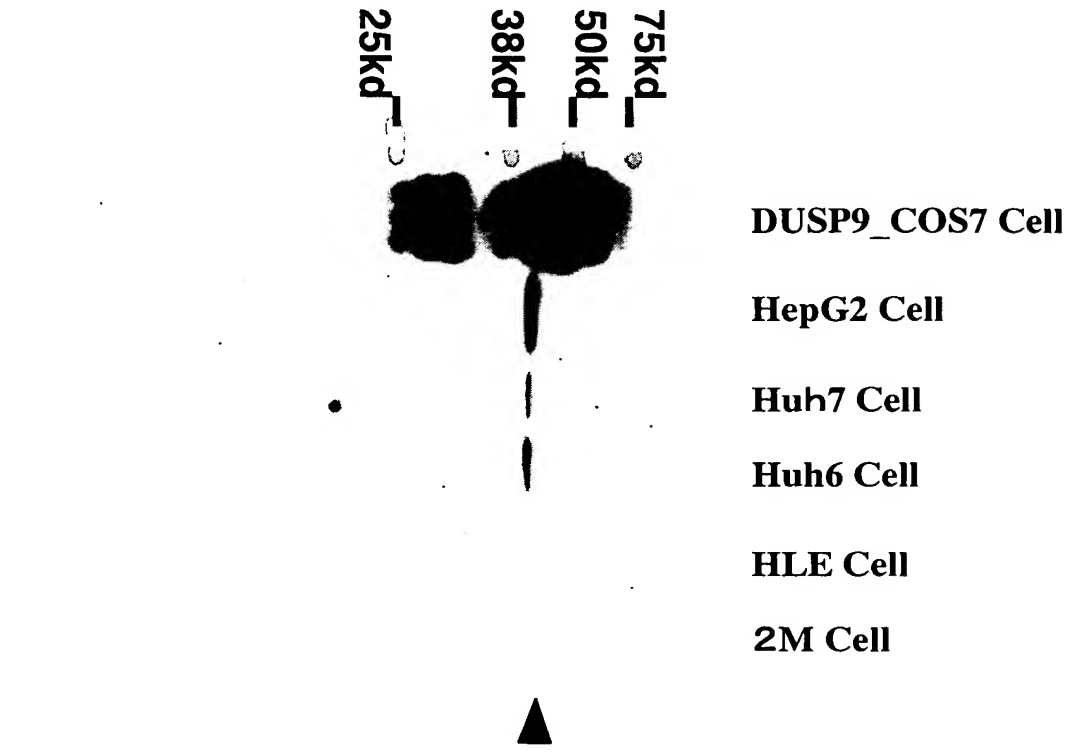

Hepatoblastoma #6
Hepatoblastoma #17
Liver cancer #16
Liver cancer #19
Liver cancer # 112
Liver cancer # 114
Liver cancer # 115
T N T N T N T N T N T N
83kDa
50kDa
PEG10/ORF2
β-actin

FIG. 83


25kd
38kd
50kd
75kd
DUSP9_COS7 Cell
HepG2 Cell
Huh7 Cell
Huh6 Cell
HLE Cell
2M Cell

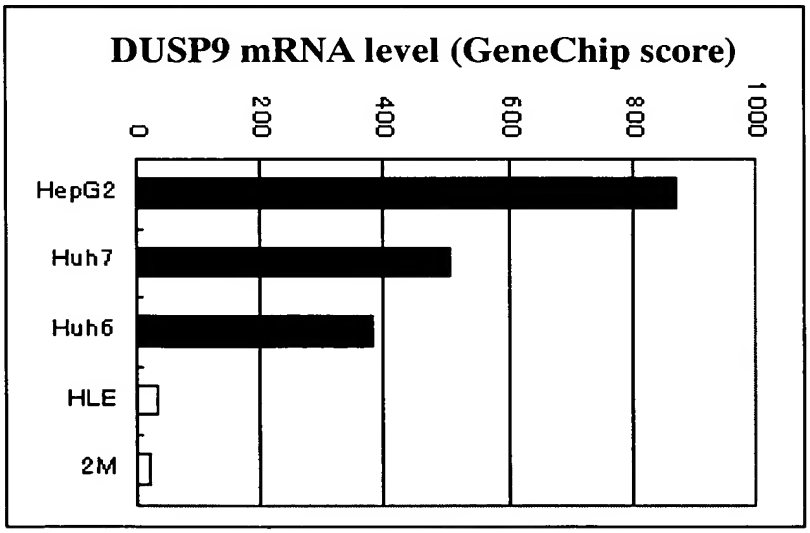

DUSP9 mRNA level (GeneChip score)
0
200
400
600
800
1000
HepG2
Huh7
Huh6
HLE
2M

FIG. 84

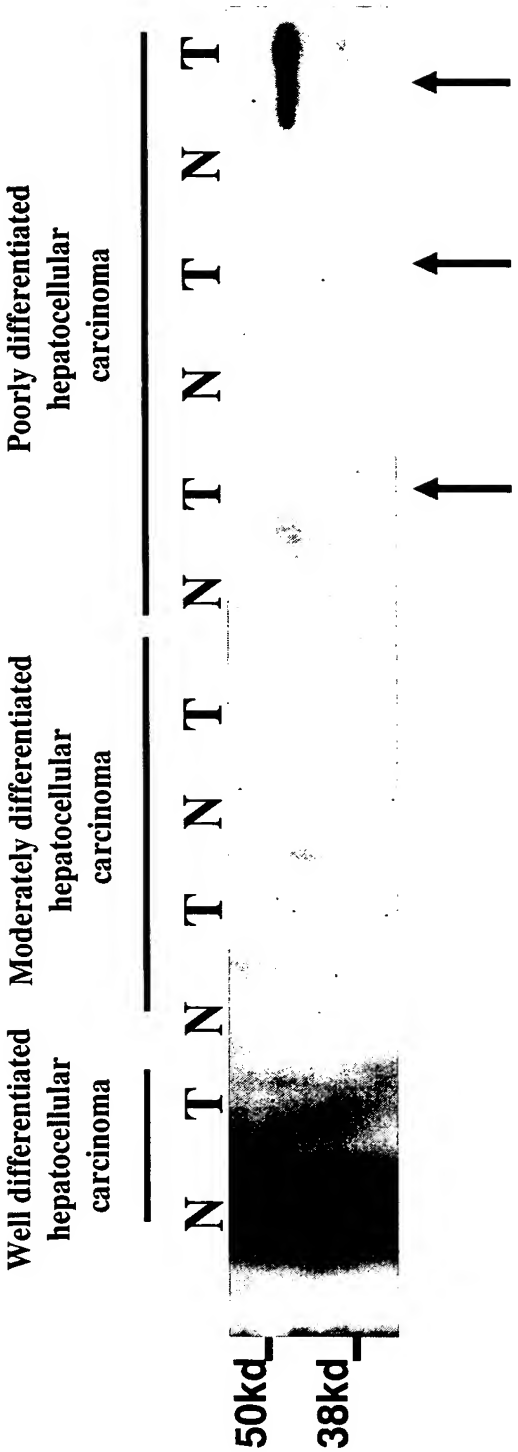

Well differentiated hepatocellular carcinoma
Moderately differentiated hepatocellular carcinoma
Poorly differentiated hepatocellular carcinoma
N T N T N T N T N T
50kd
38kd

FIG. 85

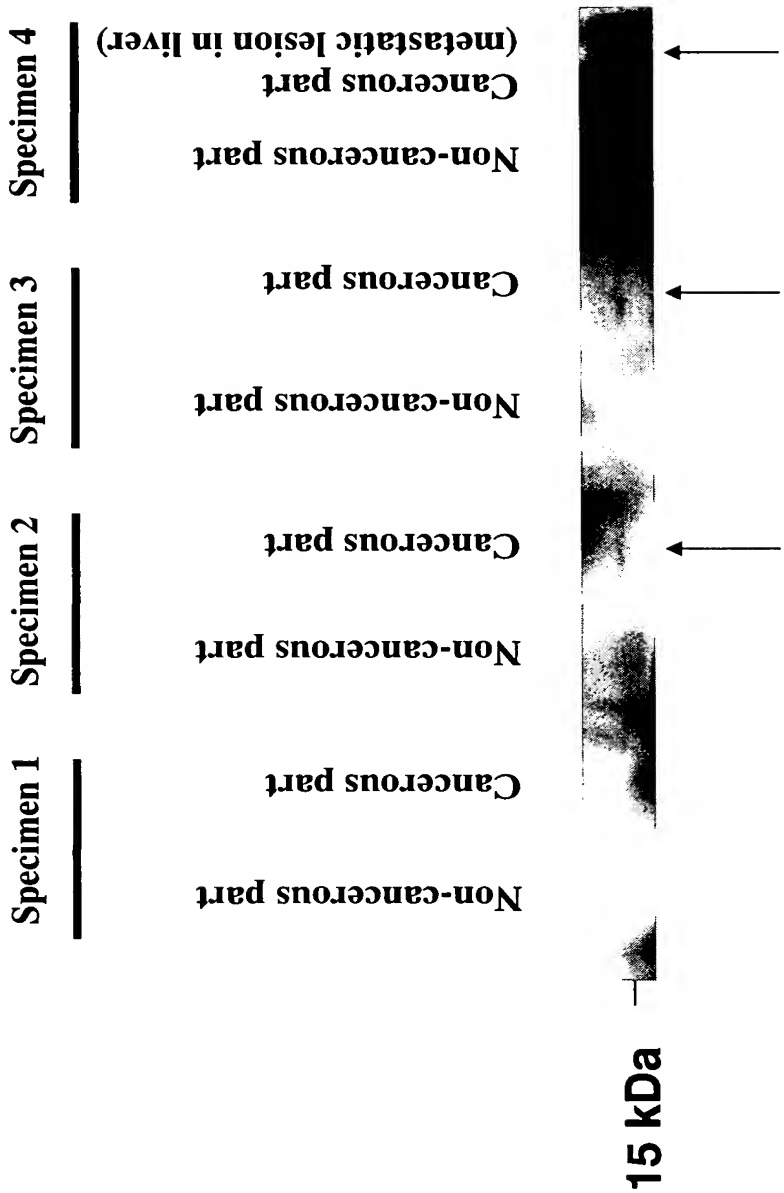

Specimen 1
Non-cancerous part
Cancerous part
Specimen 2
Non-cancerous part
Cancerous part
Specimen 3
Non-cancerous part
Cancerous part
Specimen 4
Non-cancerous part
Cancerous part
(metastatic lesion in liver)
15 kDa

FIG. 86

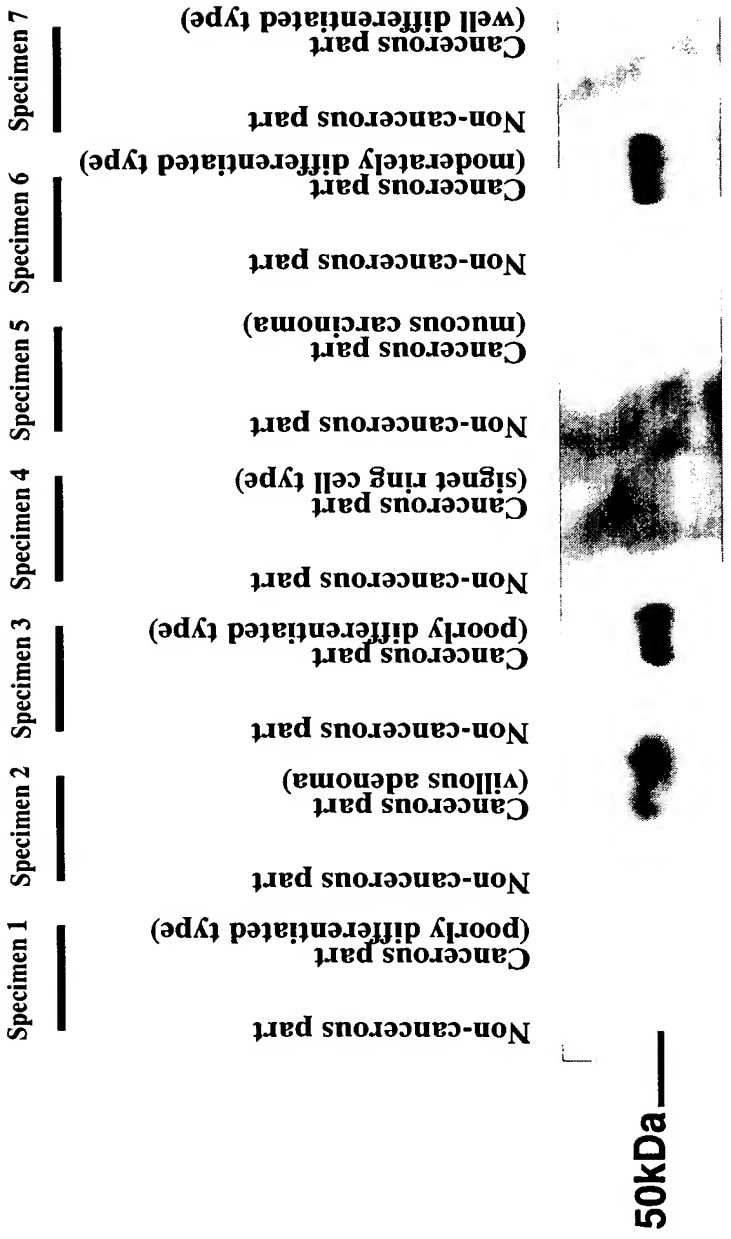

50kDa
Non-cancerous part
Cancerous part (poorly differentiated type)
Non-cancerous part
Cancerous part (villous adenoma)
Non-cancerous part
Cancerous part (poorly differentiated type)
Non-cancerous part
Cancerous part (signet ring cell type)
Non-cancerous part
Cancerous part (mucous carcinoma)
Non-cancerous part
Cancerous part (moderately differentiated type)
Non-cancerous part
Cancerous part (well differentiated type)
Specimen 1
Specimen 2
Specimen 3
Specimen 4
Specimen 5
Specimen 6
Specimen 7

FIG. 87

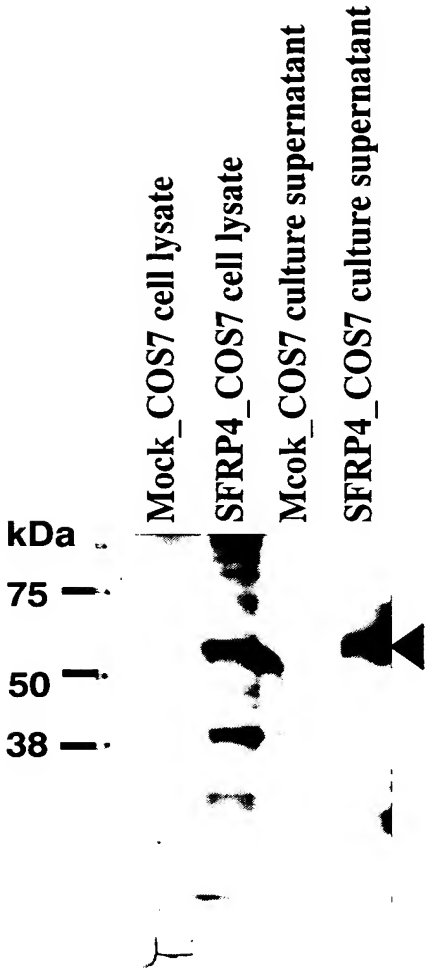

kDa
75
50
38
Mock_COS7 cell lysate
SFRP4_COS7 cell lysate
Mcok_COS7 culture supernatant
SFRP4_COS7 culture supernatant

FIG. 88